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;       FILING DATE:  28-APR-1994
;       APPLICATION NUMBER:  US 07/934,375
;       FILING DATE:  21-AUG-1992
;       APPLICATION NUMBER:  US 07/098,766
;       FILING DATE:  28-JUL-1993
;       APPLICATION NUMBER:  PCT/US93/07833
;       FILING DATE:  19-AUG-1993
;       APPLICATION NUMBER:  US 07/454,450
;       FILING DATE:  21-DEC-1989
;       APPLICATION NUMBER:  US 07/636,662
;       FILING DATE:  02-JAN-1991
;       APPLICATION NUMBER:  US 08/158,015
;       FILING DATE:  24-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haley Jr., James F.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B170 CIP 2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  385 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-450-246-58

  Query Match             47.2%;  Score 75;  DB 1;  Length 385;
  Best Local Similarity   66.7%;  Pred. No. 0.0038;
  Matches   16;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDDLEMLAPYIPM 24
              ||||||||||| |    | |  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 44
US-08-450-098-58
; Sequence 58, Application US/08450098
; Patent No. 5674980
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,098
;      FILING DATE:  25-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/235,403
;      FILING DATE:  28-APR-1994
;      APPLICATION NUMBER:  US 07/934,375
;      FILING DATE:  21-AUG-1992
;      APPLICATION NUMBER:  US 07/098,766
;      FILING DATE:  28-JUL-1993
;      APPLICATION NUMBER:  PCT/US93/07833
;      FILING DATE:  19-AUG-1993
;      APPLICATION NUMBER:  US 07/454,450
;      FILING DATE:  21-DEC-1989
;      APPLICATION NUMBER:  US 07/636,662
;      FILING DATE:  02-JAN-1991
;      APPLICATION NUMBER:  US 08/158,015
;      FILING DATE:  24-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B170 CIP 2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  385 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-450-098-58

  Query Match             47.2%;  Score 75;  DB 1;  Length 385;
  Best Local Similarity   66.7%;  Pred. No. 0.0038;
  Matches   16;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDDLEMLAPYIPM 24
              ||||||||||| |    | |  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 45
US-08-451-233-58
; Sequence 58, Application US/08451233
; Patent No. 5747641
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,233
;      FILING DATE:  25-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/235,403
;      FILING DATE:  28-APR-1994
;      APPLICATION NUMBER:  US 07/934,375
;      FILING DATE:  21-AUG-1992
;      APPLICATION NUMBER:  US 07/098,766
;      FILING DATE:  28-JUL-1993
;      APPLICATION NUMBER:  PCT/US93/07833
;      FILING DATE:  19-AUG-1993
;      APPLICATION NUMBER:  US 07/454,450
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; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-451-233-58

Query Match 47.2%; Score 75; DB 1; Length 385;
Best Local Similarity 66.7%; Pred. No. 0.0038;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAPYIPM 24
||||||||||| | | | ||
Db 2 YGRKKRRQRRRPLSQAQLMPSPPM 25

RESULT 46
US-08-450-236-58
; Sequence 58, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,236
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-236-58

Query Match 47.2%; Score 75; DB 1; Length 385;
Best Local Similarity 66.7%; Pred. No. 0.0038;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAPYIPM 24
||||||||||| | | | ||
Db 2 YGRKKRRQRRRPLSQAQLMPSPPM 25

RESULT 47
US-08-235-403-58
; Sequence 58, Application US/08235403
; Patent No. 6316003
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,403
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:

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;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;       TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  385 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-235-403-58

  Query Match             47.2%;  Score 75;  DB 3;  Length 385;
  Best Local Similarity   66.7%;  Pred. No. 0.0038;
  Matches   16;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPM 24
              |||||||||||  |    | |  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 48
US-08-706-741B-87
; Sequence 87, Application US/08706741B
; Patent No. 5955593
;  GENERAL INFORMATION:
;    APPLICANT:  KORSMEYER, STANLEY J.
;    TITLE OF INVENTION:  BH3 INTERACTING DOMAIN DEATH AGONIST
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWELL & HAFERKAMP, L.C.
;      STREET:  7733 FORSYTH BLVD., SUITE 1400
;      CITY:  ST. LOUIS
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  63146
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/706,741B
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOLLAND, DONALD R.
;      REGISTRATION NUMBER:  35,197
;      REFERENCE/DOCKET NUMBER:  965017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 727-5188
;      TELEFAX:  (314) 727-6092
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-706-741B-87

  Query Match             37.7%;  Score 60;  DB 2;  Length 32;
  Best Local Similarity   48.1%;  Pred. No. 0.038;
  Matches   13;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDD 27
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Db          1 YGRKKRRQRRRGEIIHNIARHLAQIGD 27


RESULT 49
US-08-924-695A-87
; Sequence 87, Application US/08924695A
; Patent No. 5998583
;  GENERAL INFORMATION:
;    APPLICANT:  KORSMEYER, STANLEY J.
;    TITLE OF INVENTION:  BH3 INTERACTING DOMAIN DEATH AGONIST
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWELL & HAFERKAMP, L.C.
;      STREET:  7733 FORSYTH BLVD., SUITE 1400
;      CITY:  ST. LOUIS
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  63105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/924,695A
;      FILING DATE:  09-SEP-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOLLAND, DONALD R.
;      REGISTRATION NUMBER:  35,197
;      REFERENCE/DOCKET NUMBER:  971798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 727-5188
;      TELEFAX:  (314) 727-6092
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-924-695A-87

  Query Match             37.7%;  Score 60;  DB 2;  Length 32;
  Best Local Similarity   48.1%;  Pred. No. 0.038;
  Matches   13;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

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Db          1 YGRKKRRQRRRGEIIHNIARHLAQIGD 27


RESULT 50
US-08-450-257-38
; Sequence 38, Application US/08450257
; Patent No. 5652122
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,257
;      FILING DATE:  25-MAY-1995
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;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/235,403
;       FILING DATE:  28-APR-1994
;       APPLICATION NUMBER:  US 07/934,375
;       FILING DATE:  21-AUG-1992
;       APPLICATION NUMBER:  US 07/098,766
;       FILING DATE:  28-JUL-1993
;       APPLICATION NUMBER:  PCT/US93/07833
;       FILING DATE:  19-AUG-1993
;       APPLICATION NUMBER:  US 07/454,450
;       FILING DATE:  21-DEC-1989
;       APPLICATION NUMBER:  US 07/636,662
;       FILING DATE:  02-JAN-1991
;       APPLICATION NUMBER:  US 08/158,015
;       FILING DATE:  24-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haley Jr., James F.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B170 CIP 2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  38:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  134 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-450-257-38

  Query Match             37.7%;  Score 60;  DB 1;  Length 134;
  Best Local Similarity   85.7%;  Pred. No. 0.19;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          2 YGRKKRRQRRRPPD 15


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Job time : 32.0526 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
24.205 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 159
Sequence: 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30

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Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	101	63.5	19	16	US-10-901-583-8	Sequence 8, Appli
2	101	63.5	20	14	US-10-287-670-25	Sequence 25, Appl
3	101	63.5	34	16	US-10-901-583-9	Sequence 9, Appli
4	101	63.5	54	9	US-09-922-958-5	Sequence 5, Appli
5	101	63.5	409	15	US-10-425-833-8	Sequence 8, Appli
6	101	63.5	466	15	US-10-425-833-9	Sequence 9, Appli
7	101	63.5	538	15	US-10-425-833-6	Sequence 6, Appli
8	101	63.5	542	15	US-10-264-049-2606	Sequence 2606, Ap
9	101	63.5	595	15	US-10-425-833-7	Sequence 7, Appli
10	101	63.5	632	15	US-10-425-833-10	Sequence 10, Appl
11	101	63.5	823	14	US-10-205-342-13	Sequence 13, Appl
12	101	63.5	826	9	US-09-922-958-4	Sequence 4, Appli
13	101	63.5	826	9	US-09-833-790-235	Sequence 235, App
14	101	63.5	826	9	US-09-736-457-330	Sequence 330, App
15	101	63.5	826	9	US-09-902-941-330	Sequence 330, App
16	101	63.5	826	9	US-09-849-626-330	Sequence 330, App
17	101	63.5	826	10	US-09-967-388-4	Sequence 4, Appli
18	101	63.5	826	10	US-09-476-300-330	Sequence 330, App
19	101	63.5	826	13	US-10-028-158-23	Sequence 23, Appl
20	101	63.5	826	13	US-10-101-812-10	Sequence 10, Appl
21	101	63.5	826	14	US-10-101-662A-9	Sequence 9, Appli
22	101	63.5	826	14	US-10-017-754-330	Sequence 330, App
23	101	63.5	826	14	US-10-115-987B-14	Sequence 14, Appl
24	101	63.5	826	14	US-10-287-670-9	Sequence 9, Appli
25	101	63.5	826	14	US-10-113-872-330	Sequence 330, App
26	101	63.5	826	14	US-10-423-419-2	Sequence 2, Appli
27	101	63.5	826	15	US-10-283-017-330	Sequence 330, App
28	101	63.5	826	16	US-10-901-583-18	Sequence 18, Appl
29	101	63.5	827	10	US-09-919-039-149	Sequence 149, App
30	101	63.5	827	14	US-10-247-671-137	Sequence 137, App
31	96	60.4	826	14	US-10-101-816-5	Sequence 5, Appli
32	93	58.5	826	14	US-10-101-816-2	Sequence 2, Appli
33	92	57.9	20	14	US-10-101-662A-15	Sequence 15, Appl
34	92	57.9	20	14	US-10-287-670-15	Sequence 15, Appl
35	89	56.0	19	14	US-10-313-643A-5	Sequence 5, Appli
36	89	56.0	19	14	US-10-313-551A-5	Sequence 5, Appli
37	88	55.3	826	14	US-10-101-816-6	Sequence 6, Appli
38	88	55.3	826	14	US-10-101-816-7	Sequence 7, Appli
39	87	54.7	297	15	US-10-296-115-933	Sequence 933, App
40	87	54.7	705	14	US-10-154-386-2	Sequence 2, Appli
41	76.5	48.1	205	14	US-10-121-235-2	Sequence 2, Appli
42	76.5	48.1	870	14	US-10-121-235-6	Sequence 6, Appli
43	65	40.9	169	9	US-09-981-286A-7	Sequence 7, Appli
44	64.5	40.6	195	9	US-09-949-780-6	Sequence 6, Appli
45	61.5	38.7	870	14	US-10-101-816-4	Sequence 4, Appli
46	60.5	38.1	23	13	US-10-024-935-10	Sequence 10, Appl
47	60.5	38.1	23	13	US-10-024-935-11	Sequence 11, Appl
48	60.5	38.1	23	15	US-10-603-409-10	Sequence 10, Appl
49	60.5	38.1	23	15	US-10-603-409-11	Sequence 11, Appl
50	60	37.7	22	9	US-09-949-196-8	Sequence 8, Appli
51	60	37.7	22	9	US-09-949-196-32	Sequence 32, Appl
52	60	37.7	23	14	US-10-311-111-34	Sequence 34, Appl
53	60	37.7	107	14	US-10-083-815-71	Sequence 71, Appl
54	59.5	37.4	1896	15	US-10-296-734-393	Sequence 393, App
55	59.5	37.4	5747	15	US-10-296-734-405	Sequence 405, App
56	59	37.1	685	15	US-10-369-493-611	Sequence 611, App
57	58.5	36.8	17	10	US-09-847-946A-141	Sequence 141, App
58	58.5	36.8	17	10	US-09-847-946A-142	Sequence 142, App
59	58.5	36.8	20	13	US-10-024-935-8	Sequence 8, Appli
60	58.5	36.8	20	15	US-10-603-409-8	Sequence 8, Appli
61	58.5	36.8	1893	15	US-10-296-734-399	Sequence 399, App
62	58	36.5	11	9	US-09-779-791A-1	Sequence 1, Appli
63	58	36.5	11	9	US-09-780-070-37	Sequence 37, Appl
64	58	36.5	11	9	US-09-815-108-9	Sequence 9, Appli
65	58	36.5	11	9	US-09-886-404-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-901-583-8
; Sequence 8, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09

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;  PRIOR APPLICATION NUMBER: PCT/GB00/01826
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: GB9911047.0
;  PRIOR FILING DATE: 1999-05-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Motif
US-10-901-583-8

  Query Match             63.5%;  Score 101;  DB 16;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 2
US-10-287-670-25
; Sequence 25, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., et al.
;  TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
;  TITLE OF INVENTION:  Diagnostic and
;  TITLE OF INVENTION:  Therapeutic Methods Thereof
;  FILE REFERENCE: 20363-009CIP1
;  CURRENT APPLICATION NUMBER: US/10/287,670
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 10/101,662
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 10/101,812
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 10/101,816
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-670-25

  Query Match             63.5%;  Score 101;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 3
US-10-901-583-9
; Sequence 9, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
;  APPLICANT: Ratcliffe, Peter John
;  APPLICANT:  Maxwell, Patrick Henry
;  APPLICANT:  Pugh, Christopher William
;  TITLE OF INVENTION: Interaction Between the VHL Tumour
;  TITLE OF INVENTION:  Suppressor and Hypoxia Inducible Factor, and Assay Methods
;  TITLE OF INVENTION:  Relating Thereto
;  FILE REFERENCE: 3547.1000-000
;  CURRENT APPLICATION NUMBER: US/10/901,583
;  CURRENT FILING DATE:  2004-07-29
;  PRIOR APPLICATION NUMBER: US/09/959,873
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: PCT/GB00/01826
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: GB9911047.0
;  PRIOR FILING DATE: 1999-05-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-901-583-9

  Query Match             63.5%;  Score 101;  DB 16;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db          8 DLDLEMLAPYIPMDDDFQL 26


RESULT 4
US-09-922-958-5
; Sequence 5, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
;  APPLICANT: POELLINGER, Lorenz
;  APPLICANT:  PEREIRA, Teresa
;  APPLICANT:  RUAS, Jorge
;  TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
;  TITLE OF INVENTION:  THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
;  FILE REFERENCE: 3743/49008
;  CURRENT APPLICATION NUMBER: US/09/922,958
;  CURRENT FILING DATE:  2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/223,480
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-922-958-5

  Query Match             63.5%;  Score 101;  DB 9;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db         25 DLDLEMLAPYIPMDDDFQL 43


RESULT 5
US-10-425-833-8
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; Sequence 8, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 409
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-8

  Query Match             63.5%;  Score 101;  DB 15;  Length 409;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 6
US-10-425-833-9
; Sequence 9, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

  Query Match             63.5%;  Score 101;  DB 15;  Length 466;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 7
US-10-425-833-6
; Sequence 6, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 538
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-6

  Query Match             63.5%;  Score 101;  DB 15;  Length 538;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        364 DLDLEMLAPYIPMDDDFQL 382


RESULT 8
US-10-264-049-2606
; Sequence 2606, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA133P1
;  CURRENT APPLICATION NUMBER: US/10/264,049
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/18569
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: US 60/209,467
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 4360
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2606
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-049-2606

  Query Match             63.5%;  Score 101;  DB 15;  Length 542;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        272 DLDLEMLAPYIPMDDDFQL 290


RESULT 9
US-10-425-833-7
; Sequence 7, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 595
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; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-7

Query Match 63.5%; Score 101; DB 15; Length 595;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 10
US-10-425-833-10
; Sequence 10, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
; APPLICANT: Bohl, Delphine
; APPLICANT: Heard, Jean Michael
; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
; TITLE OF INVENTION: chimeric transactivator
; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 632
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-10

Query Match 63.5%; Score 101; DB 15; Length 632;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 11
US-10-205-342-13
; Sequence 13, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Protein: hypoxia-inducible factor-1 alpha
US-10-205-342-13

Query Match 63.5%; Score 101; DB 14; Length 823;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 12
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-4

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 13
US-09-833-790-235
; Sequence 235, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-235

Query Match 63.5%; Score 101; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

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RESULT 14
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-736-457-330

  Query Match             63.5%;  Score 101;  DB 9;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 15
US-09-902-941-330
; Sequence 330, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C17
;  CURRENT APPLICATION NUMBER: US/09/902,941
;  CURRENT FILING DATE:  2001-07-10
;  NUMBER OF SEQ ID NOS: 2002
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-941-330

  Query Match             63.5%;  Score 101;  DB 9;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 16
US-09-849-626-330
; Sequence 330, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
;  APPLICANT: Bangur, Chaitanya
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Switzer, Anne
;  APPLICANT:  McNeill, Patricia
;  APPLICANT:  Clapper, Jonathan
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C16
;  CURRENT APPLICATION NUMBER: US/09/849,626
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 1926
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-626-330

  Query Match             63.5%;  Score 101;  DB 9;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 17
US-09-967-388-4
; Sequence 4, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
;  APPLICANT: JEFFEREY M. ARBEIT
;  TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
;  TITLE OF INVENTION:  WOUND HEALING
;  FILE REFERENCE: UC077.001A
;  CURRENT APPLICATION NUMBER: US/09/967,388
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-967-388-4

  Query Match             63.5%;  Score 101;  DB 10;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 18
US-09-476-300-330
; Sequence 330, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT: Bangur, Chaitanya S.
```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-300-330

Query Match 63.5%; Score 101; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 19
US-10-028-158-23
; Sequence 23, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; TITLE OF INVENTION: TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-158-23

Query Match 63.5%; Score 101; DB 13; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 20
US-10-101-812-10
; Sequence 10, Application US/10101812
; Publication No. US20020192737A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Pharmaceuticals and Methods for Treating Hypoxia and
; TITLE OF INVENTION: Screening Methods Thereof
; FILE REFERENCE: 20363-014
; CURRENT APPLICATION NUMBER: US/10/101,812
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Target Peptide
US-10-101-812-10

Query Match 63.5%; Score 101; DB 13; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 21
US-10-101-662A-9
; Sequence 9, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-662A-9

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  Query Match             63.5%;  Score 101;  DB 14;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 22
US-10-017-754-330
; Sequence 330, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C18
;  CURRENT APPLICATION NUMBER: US/10/017,754
;  CURRENT FILING DATE:  2001-10-29
;  NUMBER OF SEQ ID NOS: 2004
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-017-754-330

  Query Match             63.5%;  Score 101;  DB 14;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 23
US-10-115-987B-14
; Sequence 14, Application US/10115987B
; Publication No. US20030148521A1
; GENERAL INFORMATION:
;  APPLICANT: Bell, John C.; Stojdl, David F.;
;  APPLICANT:  Gray, Douglas A.; Sonenberg,
;  APPLICANT:  Nahum; Lichty, Brian
;  TITLE OF INVENTION: Conditionally Replicative and
;  TITLE OF INVENTION:  Conditionally Active Viruses
;  FILE REFERENCE: 42630-0001
;  CURRENT APPLICATION NUMBER: US/10/115,987B
;  CURRENT FILING DATE:  2002-03-03
;  PRIOR APPLICATION NUMBER: US60/281,781
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: EditPad
; SEQ ID NO 14
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: homo Sapiens
;  PUBLICATION INFORMATION:
;   AUTHORS: Wang et al.
;   JOURNAL: Proceedings of the National Academy of Sciences
;   VOLUME: 92
;   PAGES: 5510-5514
;   DATE: 1995
US-10-115-987B-14

  Query Match             63.5%;  Score 101;  DB 14;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 24
US-10-287-670-9
; Sequence 9, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., et al.
;  TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
;  TITLE OF INVENTION:  Diagnostic and
;  TITLE OF INVENTION:  Therapeutic Methods Thereof
;  FILE REFERENCE: 20363-009CIP1
;  CURRENT APPLICATION NUMBER: US/10/287,670
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 10/101,662
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 10/101,812
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 10/101,816
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-670-9

  Query Match             63.5%;  Score 101;  DB 14;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 25
US-10-113-872-330
; Sequence 330, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
;  APPLICANT: Watanabe, Yoshihiro
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Vedvick, Thomas S.
```

```
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C19
;  CURRENT APPLICATION NUMBER: US/10/113,872
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 2011
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-113-872-330

  Query Match             63.5%;  Score 101;  DB 14;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 26
US-10-423-419-2
; Sequence 2, Application US/10423419
; Publication No. US20030176349A1
; GENERAL INFORMATION:
;  APPLICANT: Semenza, Gregg L.
;  TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
;  TITLE OF INVENTION:  AND METHOD OF USE
;  FILE REFERENCE: JHU1500-1
;  CURRENT APPLICATION NUMBER: US/10/423,419
;  CURRENT FILING DATE:  2003-04-25
;  PRIOR APPLICATION NUMBER: US/09/383,581
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/148,547
;  PRIOR FILING DATE: 1998-08-25
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-423-419-2

  Query Match             63.5%;  Score 101;  DB 14;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 27
US-10-283-017-330
; Sequence 330, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C20
;  CURRENT APPLICATION NUMBER: US/10/283,017
;  CURRENT FILING DATE:  2002-10-28
;  NUMBER OF SEQ ID NOS: 2157
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-283-017-330

  Query Match             63.5%;  Score 101;  DB 15;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 28
US-10-901-583-18
; Sequence 18, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
;  APPLICANT: Ratcliffe, Peter John
;  APPLICANT:  Maxwell, Patrick Henry
;  APPLICANT:  Pugh, Christopher William
;  TITLE OF INVENTION: Interaction Between the VHL Tumour
;  TITLE OF INVENTION:  Suppressor and Hypoxia Inducible Factor, and Assay Methods
;  TITLE OF INVENTION:  Relating Thereto
;  FILE REFERENCE: 3547.1000-000
;  CURRENT APPLICATION NUMBER: US/10/901,583
;  CURRENT FILING DATE:  2004-07-29
;  PRIOR APPLICATION NUMBER: US/09/959,873
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: PCT/GB00/01826
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: GB9911047.0
;  PRIOR FILING DATE: 1999-05-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-901-583-18

  Query Match             63.5%;  Score 101;  DB 16;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 29
US-09-919-039-149
; Sequence 149, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
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;  SOFTWARE: PERL Program
; SEQ ID NO 149
;   LENGTH: 827
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
US-09-919-039-149

  Query Match             63.5%;  Score 101;  DB 10;  Length 827;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        557 DLDLEMLAPYIPMDDDFQL 575


RESULT 30
US-10-247-671-137
; Sequence 137, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
;  APPLICANT: Mikita, Thomas
;  APPLICANT:  Shiffman, Dov
;  APPLICANT:  Porter, Gordon, J.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
;  FILE REFERENCE: PA-0050 US
;  CURRENT APPLICATION NUMBER: US/10/247,671
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: 60/323,784
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: PERL Program
; SEQ ID NO 137
;   LENGTH: 827
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CD1
US-10-247-671-137

  Query Match             63.5%;  Score 101;  DB 14;  Length 827;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        557 DLDLEMLAPYIPMDDDFQL 575


RESULT 31
US-10-101-816-5
; Sequence 5, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-5

  Query Match             60.4%;  Score 96;  DB 14;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 6.9e-05;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||| ||||||||||||
Db        556 DLDLEMAAPYIPMDDDFQL 574


RESULT 32
US-10-101-816-2
; Sequence 2, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-2

  Query Match             58.5%;  Score 93;  DB 14;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00018;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          12 DLDLEMLAPYIPMDDDFQL 30
               ||||||||| ||||||||||
Db         556 DLDLEMLAAYIPMDDDFQL 574


RESULT 33
US-10-101-662A-15
; Sequence 15, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Livingston, David A
;  APPLICANT:  Kim, William
;  TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
;  TITLE OF INVENTION:  Therapeutic Methods Thereof
;  FILE REFERENCE: 20363-009
;  CURRENT APPLICATION NUMBER: US/10/101,662A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (9)
;   OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-101-662A-15

  Query Match             57.9%;  Score 92;  DB 14;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-06;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 DLDLEMLAPYIPMDDDFQL 30
               ||||||||| ||||||||||
Db           1 DLDLEMLAXYIPMDDDFQL 19


RESULT 34
US-10-287-670-15
; Sequence 15, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., et al.
;  TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
;  TITLE OF INVENTION:  Diagnostic and
;  TITLE OF INVENTION:  Therapeutic Methods Thereof
;  FILE REFERENCE: 20363-009CIP1
;  CURRENT APPLICATION NUMBER: US/10/287,670
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 10/101,662
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 10/101,812
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 10/101,816
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (9)
;   OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-287-670-15

  Query Match             57.9%;  Score 92;  DB 14;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-06;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 DLDLEMLAPYIPMDDDFQL 30
               ||||||||| ||||||||||
Db           1 DLDLEMLAXYIPMDDDFQL 19


RESULT 35
US-10-313-643A-5
; Sequence 5, Application US/10313643A
; Publication No. US20030153503A1
; GENERAL INFORMATION:
;  APPLICANT: Klaus, Stephen J.
;  APPLICANT:  Lin, Al Y.
;  APPLICANT:  Neff, Thomas B.
;  APPLICANT:  Wang, Qingjian
;  APPLICANT:  Arend, Michael P.
;  APPLICANT:  Flippin, Lee A.
;  APPLICANT:  Melekhov, Alexey G.
;  TITLE OF INVENTION: METHODS OF INCREASING ENDOGENOUS ERYTHROPOIETIN (EPO)
;  FILE REFERENCE: FP0601 US
;  CURRENT APPLICATION NUMBER: US/10/313,643A
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/349,659
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/386,488
;  PRIOR FILING DATE: 2002-06-05
;  PRIOR APPLICATION NUMBER: US 60/337,082
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: US 60/359,683
;  PRIOR FILING DATE: 2002-02-25
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
US-10-313-643A-5
```

```
  Query Match           56.0%;  Score 89;  DB 14;  Length 19;
  Best Local Similarity  89.5%;  Pred. No. 1.2e-05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||| |||||| ||||||
Db          1 DLDLEALAPYIPADDDFQL 19


RESULT 36
US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
;  APPLICANT: Guenzler-Pukall, Volkmar
;  APPLICANT:  Neff, Thomas B.
;  APPLICANT:  Wang, Qingjian
;  APPLICANT:  Arend, Michael
;  APPLICANT:  Flippin, Lee A.
;  APPLICANT:  Melekhov, Alexey G.
;  TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
;  FILE REFERENCE: FP0600 US
;  CURRENT APPLICATION NUMBER: US/10/313,551A
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/337,082
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: US 60/359,683
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: US 60/349,659
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/386,488
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
US-10-313-551A-5

  Query Match           56.0%;  Score 89;  DB 14;  Length 19;
  Best Local Similarity  89.5%;  Pred. No. 1.2e-05;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||| |||||| ||||||
Db          1 DLDLEALAPYIPADDDFQL 19


RESULT 37
US-10-101-816-6
; Sequence 6, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-6

  Query Match           55.3%;  Score 88;  DB 14;  Length 826;
  Best Local Similarity  89.5%;  Pred. No. 0.00092;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||| | ||||||||||
Db        556 DLDLEMAAAYIPMDDDFQL 574


RESULT 38
US-10-101-816-7
; Sequence 7, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-7

  Query Match           55.3%;  Score 88;  DB 14;  Length 826;
  Best Local Similarity  89.5%;  Pred. No. 0.00092;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||| | ||||||||||
```

```
Db        556 DLDLEMAAAYIPMDDDFQL 574


RESULT 39
US-10-296-115-933
; Sequence 933, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq Inc
;  TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 784PCT
;  CURRENT APPLICATION NUMBER: US/10/296,115
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 933
;   LENGTH: 297
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-296-115-933

  Query Match             54.7%;  Score 87;  DB 15;  Length 297;
  Best Local Similarity   94.4%;  Pred. No. 0.00043;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| |||||||
Db        166 LDLEMLAPYISMDDDFQL 183


RESULT 40
US-10-154-386-2
; Sequence 2, Application US/10154386
; Publication No. US20030026793A1
; GENERAL INFORMATION:
;  APPLICANT: Angiogene Inc.
;  APPLICANT:  Guy, Louis-Georges
;  TITLE OF INVENTION: HIPOXIA INDUCING FACTORS AND USES THEREOF FOR INDUCING ANGIOGENES
;  TITLE OF INVENTION:  IMPROVING MUSCULAR FUNCTIONS
;  FILE REFERENCE: 5600-81
;  CURRENT APPLICATION NUMBER: US/10/154,386
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: US 60/292,630
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/354529
;  PRIOR FILING DATE: 2002-02-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-154-386-2

  Query Match             54.7%;  Score 87;  DB 14;  Length 705;
  Best Local Similarity   94.4%;  Pred. No. 0.0011;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| |||||||
Db        521 LDLEMLAPYISMDDDFQL 538


RESULT 41
US-10-121-235-2
; Sequence 2, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT:  Maemura, Koji
;  APPLICANT:  Hsieh, Chung-Ming
;  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
;  FILE REFERENCE: 05433/037001
;  CURRENT APPLICATION NUMBER: US/10/121,235
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/374,454
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: US 60/096,515
;  PRIOR FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-121-235-2

  Query Match             48.1%;  Score 76.5;  DB 14;  Length 205;
  Best Local Similarity   80.0%;  Pred. No. 0.0088;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db         38 ELDLETLAPYIPMDGEDFQL 57


RESULT 42
US-10-121-235-6
; Sequence 6, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT:  Maemura, Koji
;  APPLICANT:  Hsieh, Chung-Ming
;  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
;  FILE REFERENCE: 05433/037001
;  CURRENT APPLICATION NUMBER: US/10/121,235
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/374,454
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: US 60/096,515
;  PRIOR FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 870
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-121-235-6

  Query Match             48.1%;  Score 76.5;  DB 14;  Length 870;
  Best Local Similarity   80.0%;  Pred. No. 0.041;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 43
US-09-981-286A-7
; Sequence 7, Application US/09981286A
; Publication No. US20020192799A1
; GENERAL INFORMATION:
;  APPLICANT: Watowich, Stanley J.
;  APPLICANT:  Weaver, Scott C.
;  APPLICANT:  Davey, Robert A.
;  TITLE OF INVENTION: Drug Discovery Methods
;  FILE REFERENCE: 265.00260101
;  CURRENT APPLICATION NUMBER: US/09/981,286A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: US 60/240,187
;  PRIOR FILING DATE: 2000-10-13
```

```
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of tat-CCD
US-09-981-286A-7

  Query Match             40.9%;  Score 65;  DB 9;  Length 169;
  Best Local Similarity   81.2%;  Pred. No. 0.3;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDDLE 16
              ||||||||||| : ||
Db          2 YGRKKRRQRRRVMKLE 17


RESULT 44
US-09-949-780-6
; Sequence 6, Application US/09949780
; Patent No. US20020061296A1
; GENERAL INFORMATION:
;  APPLICANT: No. US20020061296A1eborn, Mathieu H.M.
;  APPLICANT:  Voorhoeve, Pieter M.
;  APPLICANT:  Zhang, Ying-Hui
;  APPLICANT:  Leliveld, Sirik R.
;  TITLE OF INVENTION: A Delivery Method for the Tumor Specific Apoptosis Inducing Activ
;  TITLE OF INVENTION:  Apoptin
;  FILE REFERENCE: 2906-5001.1US
;  CURRENT APPLICATION NUMBER: US/09/949,780
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: US 60/236,117
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 195
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence of XNvp3
US-09-949-780-6

  Query Match             40.6%;  Score 64.5;  DB 9;  Length 195;
  Best Local Similarity   66.7%;  Pred. No. 0.41;
  Matches   14;  Conservative    1;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDDLEMLAPY 21
              ||||||||||||   : |  ||
Db         38 YGRKKRRQRRRG-QISMAYPY 57


RESULT 45
US-10-101-816-4
; Sequence 4, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 870
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-4

  Query Match             38.7%;  Score 61.5;  DB 14;  Length 870;
  Best Local Similarity   70.0%;  Pred. No. 5.4;
  Matches   14;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| || ||||| : |||
Db        523 ELDLETLAAYIPMDGEGFQL 542


RESULT 46
US-10-024-935-10
; Sequence 10, Application US/10024935
; Publication No. US20020142966A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth Walter Bair
;  APPLICANT:  YingNan Pan Chen
;  APPLICANT:  Timothy Michael Ramsey
;  APPLICANT:  Michael Lloyd Sabio
;  APPLICANT:  Sushill  Kumar Sharma
;  TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
;  TITLE OF INVENTION:  Interaction for Cancer Therapy
;  FILE REFERENCE: 4-31664P1/Prov
;  CURRENT APPLICATION NUMBER: US/10/024,935
;  CURRENT FILING DATE:  2001-12-19
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-024-935-10

  Query Match             38.1%;  Score 60.5;  DB 13;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 0.16;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRD-LDL 15
              |||||||||||  |||
Db          1 YGRKKRRQRRRGRLDL 16


RESULT 47
US-10-024-935-11
; Sequence 11, Application US/10024935
; Publication No. US20020142966A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth Walter Bair
;  APPLICANT:  YingNan Pan Chen
;  APPLICANT:  Timothy Michael Ramsey
;  APPLICANT:  Michael Lloyd Sabio
```

```
;  APPLICANT:  Sushill  Kumar Sharma
;  TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
;  TITLE OF INVENTION:  Interaction for Cancer Therapy
;  FILE REFERENCE: 4-31664P1/Prov
;  CURRENT APPLICATION NUMBER: US/10/024,935
;  CURRENT FILING DATE:  2001-12-19
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-024-935-11

  Query Match             38.1%;  Score 60.5;  DB 13;  Length 23;
  Best Local Similarity   70.0%;  Pred. No. 0.16;
  Matches   14;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLA 19
              |||||||||||  : | : ||
Db          1 YGRKKRRQRRRGETDHQYLA 20


RESULT 48
US-10-603-409-10
; Sequence 10, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth Walter Bair
;  APPLICANT:  YingNan Pan Chen
;  APPLICANT:  Timothy Michael Ramsey
;  APPLICANT:  Michael Lloyd Sabio
;  APPLICANT:  Sushill  Kumar Sharma
;  TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
;  TITLE OF INVENTION:  Interaction for Cancer Therapy
;  FILE REFERENCE: 4-33243/P1/N1
;  CURRENT APPLICATION NUMBER: US/10/603,409
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: 10/024,935
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: PCT/EP1 /15006
;  PRIOR FILING DATE: 2001-12-19
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-10

  Query Match             38.1%;  Score 60.5;  DB 15;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 0.16;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRD-LDL 15
              |||||||||||  |||
Db          1 YGRKKRRQRRRGRLDL 16


RESULT 49
US-10-603-409-11
; Sequence 11, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth Walter Bair
;  APPLICANT:  YingNan Pan Chen
;  APPLICANT:  Timothy Michael Ramsey
;  APPLICANT:  Michael Lloyd Sabio
;  APPLICANT:  Sushill  Kumar Sharma
;  TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
;  TITLE OF INVENTION:  Interaction for Cancer Therapy
;  FILE REFERENCE: 4-33243/P1/N1
;  CURRENT APPLICATION NUMBER: US/10/603,409
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: 10/024,935
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: PCT/EP1 /15006
;  PRIOR FILING DATE: 2001-12-19
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-11

  Query Match             38.1%;  Score 60.5;  DB 15;  Length 23;
  Best Local Similarity   70.0%;  Pred. No. 0.16;
  Matches   14;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLA 19
              |||||||||||  : | : ||
Db          1 YGRKKRRQRRRGETDHQYLA 20


RESULT 50
US-09-949-196-8
; Sequence 8, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
;  APPLICANT: Zealand Pharmaceuticals A/S
;  TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE
;  TITLE OF INVENTION:  TO DNA DAMAGE
;  FILE REFERENCE: 55888 (45487)
;  CURRENT APPLICATION NUMBER: US/09/949,196
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (22)..(22)
;   OTHER INFORMATION: NH2
US-09-949-196-8

  Query Match             37.7%;  Score 60;  DB 9;  Length 22;
  Best Local Similarity   85.7%;  Pred. No. 0.18;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLD 14
              ||||||||||  |
Db          1 YGRKKRRQRRRLFD 14


Search completed: February  9, 2005, 06:35:43
Job time : 404.684 secs
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OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 166.842 Seconds
(without alignments)
69.544 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 159
Sequence: 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	100.0	30	6	ABR82380	Abr82380 Hypoxia-i
2	144	90.6	1125	6	ABP57672	Abp57672 HIF-1 alp
3	144	90.6	1160	6	ABP57674	Abp57674 HIF-1 alp
4	142.5	89.6	1087	6	ABP57673	Abp57673 HIF-1 alp
5	142.5	89.6	1122	6	ABP57675	Abp57675 HIF-1 alp
6	124	78.0	28	7	AAO23532	Aao23532 Fluoresce
7	101	63.5	19	4	AAB49912	Aab49912 Human/mur
8	101	63.5	19	6	AAE30167	Aae30167 Peptide #
9	101	63.5	19	6	AAE30144	Aae30144 HIFalpha
10	101	63.5	19	6	AAE30162	Aae30162 Peptide #
11	101	63.5	19	6	AAE30172	Aae30172 Human HIF
12	101	63.5	19	6	AAE30158	Aae30158 HIF-1alph
13	101	63.5	19	6	ABR82378	Abr82378 Hypoxia-i
14	101	63.5	19	8	ADP56728	Adp56728 Substrate
15	101	63.5	19	8	ADP79479	Adp79479 Hypoxia i
16	101	63.5	20	6	ABP55440	Abp55440 Hypoxia-i
17	101	63.5	20	8	ADO22337	Ado22337 HIF-1alph
18	101	63.5	29	7	AAO23481	Aao23481 Murine HI
19	101	63.5	29	7	AAO23499	Aao23499 Murine HI
20	101	63.5	34	4	AAB49913	Aab49913 Human/mur
21	101	63.5	34	6	AAE30161	Aae30161 Peptide #
22	101	63.5	34	6	AAE30151	Aae30151 HIFalpha
23	101	63.5	54	3	AAY94637	Aay94637 HIF-1alph
24	101	63.5	54	7	AAO23490	Aao23490 Murine HI
25	101	63.5	54	7	AAO23530	Aao23530 Murine HI
26	101	63.5	54	7	AAO23528	Aao23528 Murine HI
27	101	63.5	54	7	AAO23529	Aao23529 Murine HI
28	101	63.5	116	3	AAY94632	Aay94632 HIF-1alph
29	101	63.5	288	3	AAY94633	Aay94633 HIF-1alph
30	101	63.5	301	3	AAY94634	Aay94634 HIF-1alph
31	101	63.5	311	3	AAY94631	Aay94631 HIF-1alph
32	101	63.5	409	8	ADO39389	Ado39389 Chimeric
33	101	63.5	444	4	AAB68415	Aab68415 Amino aci
34	101	63.5	466	8	ADO39390	Ado39390 Chimeric
35	101	63.5	538	8	ADO39387	Ado39387 Chimeric
36	101	63.5	542	5	ABP41474	Abp41474 Human ova
37	101	63.5	595	8	ADO39388	Ado39388 Chimeric
38	101	63.5	613	3	AAY94630	Aay94630 HIF-1alph
39	101	63.5	613	5	AAU77614	Aau77614 Human hyp
40	101	63.5	632	8	ADO39391	Ado39391 Chimeric
41	101	63.5	652	3	AAY94629	Aay94629 HIF-1alph
42	101	63.5	669	3	AAY84167	Aay84167 A variant
43	101	63.5	697	3	AAY84166	Aay84166 A variant
44	101	63.5	701	3	AAY84173	Aay84173 A variant
45	101	63.5	710	3	AAY84172	Aay84172 A variant
46	101	63.5	724	3	AAY84171	Aay84171 A variant
47	101	63.5	735	6	ABR82375	Abr82375 Hypoxia-i
48	101	63.5	735	8	ADN75066	Adn75066 Human hyp
49	101	63.5	749	3	AAY84170	Aay84170 A variant
50	101	63.5	756	3	AAY94635	Aay94635 HIF-1alph
51	101	63.5	789	3	AAY84169	Aay84169 A variant
52	101	63.5	789	6	ADA18535	Ada18535 Human hyp
53	101	63.5	789	6	ADA18533	Ada18533 Human hyp
54	101	63.5	789	6	ADA18534	Ada18534 Human hyp
55	101	63.5	805	2	AAW06558	Aaw06558 Hypoxia i
56	101	63.5	810	5	ABB57270	Abb57270 Mouse isc
57	101	63.5	813	3	AAY94636	Aay94636 HIF-1alph
58	101	63.5	823	6	ABR41951	Abr41951 Rat hypox
59	101	63.5	825	7	ADD44855	Add44855 Rat Prote
60	101	63.5	826	2	AAW06557	Aaw06557 Human hyp
61	101	63.5	826	2	AAW80418	Aaw80418 Amino aci
62	101	63.5	826	2	AAY06289	Aay06289 Human tra
63	101	63.5	826	3	AAY69407	Aay69407 A wild ty
64	101	63.5	826	3	AAY94640	Aay94640 Human hyp
65	101	63.5	826	4	AAB76854	Aab76854 Human lun

ALIGNMENTS

RESULT 1
ABR82380
ID ABR82380 standard; peptide; 30 AA.
XX
AC ABR82380;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hypoxia-inducible factor 1 (HIF-1) alpha inhibitor ODD peptide.
XX
KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquillizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /label= Hyp
FT /note= "hydroxyproline"
XX
PN WO2003057820-A2.
XX
PD 17-JUL-2003.
XX
PF 04-OCT-2002; 2002WO-US031699.
XX
PR 21-DEC-2001; 2001US-00032361.

XX
PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
XX
PI Mcgrath K;
XX
DR WPI; 2003-645988/61.
XX
PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX
PS Claim 2; Page 9; 37pp; English.
XX
CC The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC an ODD peptide, a specific example of HIF-1 alpha peptide inhibitor,
CC containing the oxygen-dependent degradation sequence of HIF-1 alpha
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 159; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||||||||||||
Db 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30

RESULT 2
ABP57672
ID ABP57672 standard; protein; 1125 AA.
XX
AC ABP57672;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pCH/TAT/3-0 SEQ ID NO:39.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76624.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX
PS Example 3; Page 75-78; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1125 AA;

Query Match 90.6%; Score 144; DB 6; Length 1125;
Best Local Similarity 75.0%; Pred. No. 1.8e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 1 YGRKKRRQRRR----------DLDLEMLAPYIPMDDDFQL 30
||||||||||| ||||||||||||||||||
Db 11 YGRKKRRQRRRRSNPFSTQDTDLDLEMLAPYIPMDDDFQL 50

RESULT 3
ABP57674
ID ABP57674 standard; protein; 1160 AA.
XX
AC ABP57674;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pBAD/3-0 SEQ ID NO:43.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76626.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer

PT and improvement of microbial fermentation.
XX
PS Example 3; Page 95-99; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1160 AA;

Query Match 90.6%; Score 144; DB 6; Length 1160;
Best Local Similarity 75.0%; Pred. No. 1.9e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

```
Qy          1 YGRKKRRQRRR----------DLDLEMLAPYIPMDDDFQL 30
              ||||||||||          ||||||||||||||||||||
Db         46 YGRKKRRQRRRRSNPFSTQDTDLDLEMLAPYIPMDDDFQL 85
```

RESULT 4
ABP57673
ID ABP57673 standard; protein; 1087 AA.
XX
AC ABP57673;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pCH/TAT/557-574 SEQ ID NO:41.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76625.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX
PS Example 3; Page 85-88; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1087 AA;

Query Match 89.6%; Score 142.5; DB 6; Length 1087;
Best Local Similarity 93.5%; Pred. No. 2.9e-11;
Matches 29; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 YGRKKRRQ-RRRDLDLEMLAPYIPMDDDFQL 30
              |||||||| ||| ||||||||||||||||||
Db         11 YGRKKRRQRRRRSLDLEMLAPYIPMDDDFQL 41
```

RESULT 5
ABP57675
ID ABP57675 standard; protein; 1122 AA.
XX
AC ABP57675;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pBAD/557-574 SEQ ID NO:45.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76627.
XX

```
PT   New DNA encoding a polypeptide imparting relative stability under hypoxic
PT   conditions to proteins within the cell, useful for treatment of cancer
PT   and improvement of microbial fermentation.
XX
PS   Example 3; Page 106-109; 144pp; Japanese.
XX
CC   The present invention describes DNA encoding a hypoxia-inducible factor 1
CC   alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC   see ABP57669) (I), or encoding a fusion protein containing at least 16
CC   residues of (I), a nuclear localisation signal (NLS), and another
CC   protein, and imparting relative stability under specific conditions of
CC   oxygen concentration within the cell. Also described: (1) vectors
CC   containing the DNA; (2) cells transformed by the vectors; (3) producing
CC   the fusion protein by culture of the transformed cells; (4) detecting
CC   hypoxic conditions in cells by monitoring the stability of the protein
CC   fused to (I) in cells transformed by vectors containing the DNA; (5)
CC   regulating the stability of proteins within the cell by transformation
CC   with the DNA; (6) inhibiting the development of cells under hypoxic
CC   conditions, using the fusion protein; (7) fusion proteins encoded by the
CC   DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC   tension. (I) has cytostatic activity, and can be used for the
CC   stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC   solid tumour, and in gene therapy. (I) can be used in industrial
CC   microbial fermentation, and in medicine, especially in the treatment of
CC   tumours containing hypoxic regions. The present sequence represents a
CC   fusion protein from the present invention
XX
SQ   Sequence 1122 AA;

  Query Match             89.6%;  Score 142.5;  DB 6;  Length 1122;
  Best Local Similarity   93.5%;  Pred. No. 3e-11;
  Matches   29;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQ-RRRDLDLEMLAPYIPMDDDFQL 30
              |||||||| ||| ||||||||||||||||||
Db         46 YGRKKRRQRRRRSLDLEMLAPYIPMDDDFQL 76


RESULT 6
AAO23532
ID   AAO23532 standard; peptide; 28 AA.
XX
AC   AAO23532;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Fluorescein HIV-TAT cellular uptake signal-HIF-1alpha peptide 2.
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; HIV; tat;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1. .13
FT                    /note= "HIV-TAT cellular uptake signal peptide"
FT   Modified-site    1
FT                    /note= "5'- fluorescein label"
FT   Peptide          14. .28
FT                    /note= "HIF-1alpha mutant peptide"
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Example 16; Fig 32; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. The present sequence represents a HIF-1alpha
CC   mutant peptide linked to a fluorescein labeled HIV-TAT cellular uptake
CC   signal peptide
XX
SQ   Sequence 28 AA;

  Query Match             78.0%;  Score 124;  DB 7;  Length 28;
  Best Local Similarity   86.7%;  Pred. No. 2.5e-10;
  Matches   26;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30
              ||||||||||    ||||||||||||||
Db          1 YGRKKRRQRRR--PPEMLAPYIPMDDDFQL 28


RESULT 7
AAB49912
ID   AAB49912 standard; peptide; 19 AA.
XX
AC   AAB49912;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Human/murine HIF-1alpha subunit conserved motif #8.
XX
KW   Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
KW   hypoxia inducible factor-1; cancer; ischaemia.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO200069908-A1.
XX
PD   23-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-GB001826.
XX
PR   12-MAY-1999;   99GB-00011047.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Ratcliffe PJ,  Maxwell PH,  Pugh CW;
XX
DR   WPI; 2001-025006/03.
XX
PT   Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
PT   subunit interaction modulators for treating ischemia by contacting a VHL
PT   protein and an HIF subunit protein with a putative modulator.
```

XX
PS Claim 13; Page 49; 56pp; English.
XX
CC The present invention describes a novel assay for use in identifying
CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
CC contacting the VHL protein, the HIF-1alpha subunit and the putative
CC modulator under conditions where the former two would normally complex.
CC Modulators of this type are useful in the treatment of cancer and
CC ischaemic conditions such as coronary, cerebral and vascular
CC insufficiency
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 8
AAE30167
ID AAE30167 standard; peptide; 19 AA.
XX
AC AAE30167;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #7 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS Unidentified.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 247; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 9
AAE30144
ID AAE30144 standard; peptide; 19 AA.
XX
AC AAE30144;
XX
DT 24-FEB-2003 (first entry)
XX
DE HIFalpha subunit antagonist #1.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW antagonist.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 2
FT /label= Hyp
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Claim 49; Page 196; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is HIFalpha subunit antagonist. This
CC sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 6; Length 19;

```
  Best Local Similarity   100.0%;  Pred. No. 3e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 10
AAE30162
ID   AAE30162 standard; peptide; 19 AA.
XX
AC   AAE30162;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Peptide #2 used to block HIF-1alpha/pVHL interaction.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Example 1; Page 246; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC   interaction. This sequence is used in the invention
XX
SQ   Sequence 19 AA;

  Query Match             63.5%;  Score 101;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 11
AAE30172
ID   AAE30172 standard; peptide; 19 AA.
XX
AC   AAE30172;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human HIF1-alpha peptide #2.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW   human; HIF1-alpha.
XX
OS   Homo sapiens.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Disclosure; Page 252; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is human HIF1-alpha peptide. This sequence
CC   is used in the invention
XX
SQ   Sequence 19 AA;

  Query Match             63.5%;  Score 101;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 12
AAE30158
ID   AAE30158 standard; peptide; 19 AA.
XX
AC   AAE30158;
XX
DT   24-FEB-2003  (first entry)
XX
DE   HIF-1alpha pVHL minimal binding domain.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
```

KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW human.
XX
OS Homo sapiens.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 245; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is HIF-1alpha pVHL minimal binding domain.
CC This sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 13
ABR82378
ID ABR82378 standard; peptide; 19 AA.
XX
AC ABR82378;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hypoxia-inducible factor 1 (HIF-1) alpha peptide inhibitor.
XX
KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquillizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /label= Hyp
FT /note= "hydroxyproline"
XX
PN WO2003057820-A2.
XX
PD 17-JUL-2003.
XX
PF 04-OCT-2002; 2002WO-US031699.
XX
PR 21-DEC-2001; 2001US-00032361.
XX
PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
XX
PI Mcgrath K;
XX
DR WPI; 2003-645988/61.
XX
PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX
PS Claim 2; Page 8; 37pp; English.
XX
CC The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC a specific example of HIF-1 alpha peptide inhibitor, containing the
CC oxygen-dependent degradation sequence of HIF-1 alpha
XX
SQ Sequence 19 AA;

Query Match 63.5%; Score 101; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 14
ADP56728
ID ADP56728 standard; peptide; 19 AA.
XX
AC ADP56728;
XX
DT 09-SEP-2004 (first entry)
XX
DE Substrate peptide used in human HIF prolyl hydroxylase screening assay.
XX
KW fat metabolism; HIFalpha; hypoxia inducible factor alpha subunit;
KW atherosclerosis; diabetes; obesity; HIF prolyl hydroxylase substrate;
KW human; HIF-PH.
XX
OS Homo sapiens.
XX
PN WO2004052285-A2.
XX
PD 24-JUN-2004.
XX
PF 05-DEC-2003; 2003WO-US038690.
XX
PR 06-DEC-2002; 2002US-0431351P.
PR 06-JUN-2003; 2003US-0476331P.
PR 06-JUN-2003; 2003US-0476726P.
PR 04-DEC-2003; 2003US-00729167.
XX
PA (FIBR-) FIBROGEN INC.
XX
PI Fourney PD, Guenzler-Pukall V, Klaus SJ, Lin AY, Neff TB;
PI Seeley TW;

```
XX
DR   WPI; 2004-468689/44.
XX
PT   Regulating fat metabolism or fat metabolic process in subjects, by
PT   stabilizing human foreskin fibroblasts alpha in subject, thus regulating
PT   fat metabolism or fat metabolic process in subject.
XX
PS   Example 9; SEQ ID NO 1; 66pp; English.
XX
CC   The invention relates to a novel method for regulating fat metabolism or
CC   the fat metabolic process in a subject which comprises stabilising human
CC   foreskin fibroblast HIFalpha (hypoxia inducible factor alpha subunit) in
CC   the subject, or administering a compound that inhibits HIF hydroxylase
CC   activity, thus regulating fat metabolism or the fat metabolic process in
CC   the subject. The method of the invention may be useful for regulating fat
CC   metabolism or a fat metabolic process in a subject. The subject is an
CC   animal, preferably a mammal, more preferably human and the method is
CC   performed in a human cell, tissue or organ. The method may be useful for
CC   treating or preventing atherosclerosis, diabetes and obesity in a
CC   subject. The current sequence is that of the substrate peptide of the
CC   invention which is used during a screening assay of human HIF prolyl
CC   hydroxylase (HIF-PH).
XX
SQ   Sequence 19 AA;

  Query Match             63.5%;  Score 101;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 15
ADP79479
ID   ADP79479 standard; peptide; 19 AA.
XX
AC   ADP79479;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Hypoxia inducible factor prolyl hydroxylase substrate peptide.
XX
KW   Human; Hypoxia inducible factor prolyl hydroxylase; glucose metabolism;
KW   antidiabetic; anorectic; hypotensive; antilipaemic; nephrotropic;
KW   neuroprotective; ophthalmological; antiarteriosclerotic; vasotropic;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2004052284-A2.
XX
PD   24-JUN-2004.
XX
PF   05-DEC-2003; 2003WO-US038689.
XX
PR   06-DEC-2002; 2002US-0431351P.
PR   06-JUN-2003; 2003US-0476331P.
PR   06-JUN-2003; 2003US-0476726P.
PR   04-DEC-2003; 2003US-00729704.
XX
PA   (FIBR-) FIBROGEN INC.
XX
PI   Guenzler-Pukall V,  Klaus SJ,  Langsetmo Parobok I,  Seeley TW;
XX
DR   WPI; 2004-468688/44.
XX
PT   Regulating glucose metabolism or glucose metabolic process in subject,
PT   involves stabilizing hypoxia inducible factor alpha in subject, or
PT   administering to subject compound inhibiting hypoxia inducible factor
PT   hydroxylase activity.
XX
PS   Example 14; SEQ ID NO 5; 74pp; English.
XX
CC   The present sequence is that of a substrate peptide for hypoxia inducible
CC   factor (HIF) prolyl hydroxylase. It was used in an example from the
CC   invention for the identification of compounds useful for HIF alpha
CC   stabilisation. The invention provides methods and compounds for
CC   regulating glucose metabolism by stabilising HIF alpha, especially by
CC   administering a compound that inhibits HIF hydroxylase activity. The
CC   method of stabilising HIF alpha is used in claimed methods for achieving
CC   glucose homeostasis, decreasing blood glucose levels, decreasing glycated
CC   haemoglobin levels, altering expression of a glucose regulatory factor,
CC   altering expression of a glycolytic factor, treating or preventing
CC   diabetes, treating or preventing a disorder associated with increased
CC   blood glucose levels (especially diabetes, hyperglycaemia, obesity,
CC   hypertension, hyperlipidaemia, nephropathy, neuropathy, retinopathy,
CC   impaired glucose tolerance, atherosclerosis and vascular disease),
CC   treating or preventing a condition associated with diabetes, decreasing
CC   blood triglyceride levels, reducing insulin resistance, and increasing
CC   glycaemic control in a subject.
XX
SQ   Sequence 19 AA;

  Query Match             63.5%;  Score 101;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 16
ABP55440
ID   ABP55440 standard; peptide; 20 AA.
XX
AC   ABP55440;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Hypoxia-inducible factor (HIF) 1 alpha peptide.
XX
KW   Hypoxia; hypoxia-inducible factor; HIF1-alpha; hypoxic-related disorder;
KW   ischaemic-related disorder; hypoxia-inducible factor-related disorder;
KW   prolyl hydroxylation; HIF; hypoxic; ischaemic; vasotropic; cardiant;
KW   cerebroprotective; cytostatic; thrombolytic; antidiabetic; nephrotropic;
KW   myocardial infarction; heart disease; stroke; cancer; diabetes;
KW   cell-proliferating disorder; deep vein thrombosis; pulmonary embolus;
KW   renal failure; angiogenesis; vascularisation; prolyl hydroxylase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   9
FT                   /label= hydroxyproline
XX
PN   WO200274249-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US008886.
XX
PR   20-MAR-2001; 2001US-0277425P.
PR   20-MAR-2001; 2001US-0277431P.
PR   20-MAR-2001; 2001US-0277440P.
PR   09-NOV-2001; 2001US-0332334P.
PR   09-NOV-2001; 2001US-0332493P.
PR   09-NOV-2001; 2001US-0345200P.
PR   20-DEC-2001; 2001US-0342598P.
PR   20-DEC-2001; 2001US-0345131P.
PR   20-DEC-2001; 2001US-0345132P.
PR   19-MAR-2002; 2002US-00101812.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
```

XX
PI Kaelin WG, Ivan M;
XX
DR WPI; 2003-058330/05.
XX
PT Treating or preventing a hypoxic- or ischemic-related disorder, e.g.
PT myocardial infarction, stroke, cancer, thrombosis or renal failure, by
PT administering a modulator prolyl hydroxylation of hypoxia-inducible
PT factor (HIF).
XX
PS Disclosure; Page 26; 128pp; English.
XX
CC The present invention describes a method for treating or preventing a
CC hypoxic-related disorder, ischaemic-related disorder, or hypoxia-
CC inducible factor (HIF)-related disorder in a subject by administering to
CC the subject a compound that modulates prolyl hydroxylation of HIF, such
CC that the hypoxic-, ischaemic-, or HIF-related disorder is treated,
CC prevented, reversed or stabilised. HIF related sequences can have
CC vasotropic, cardiant, cerebroprotective, cytostatic, thrombolytic,
CC antidiabetic, and nephrotropic activities. The method is useful for
CC treating hypoxia-related disorder, ischaemic-related disorder or HIF-
CC related disorder. In particular, the hypoxic- or ischaemic-related
CC disorder is an acute event (e.g. myocardial infarction, heart disease,
CC stroke, cancer or cell-proliferating disorder, or diabetes) or a chronic
CC event (e.g. deep vein thrombosis, pulmonary embolus or renal failure),
CC especially a chronic event not caused by tissue scarring. The method is
CC also useful for increasing angiogenesis or vascularisation. The present
CC sequence represents a human hypoxia-inducible factor 1 alpha (HIF1-alpha)
CC peptide which is given in the exemplification of the present invention
XX
SQ Sequence 20 AA;

Query Match 63.5%; Score 101; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 17
ADO22337
ID ADO22337 standard; peptide; 20 AA.
XX
AC ADO22337;
XX
DT 12-AUG-2004 (first entry)
XX
DE HIF-1alpha ligand binding site peptide SEQ ID NO:15.
XX
KW transgenic; transgenic non-human animal; light-generating fusion protein;
KW ligand binding site; light-generating polypeptide moiety;
KW hypoxia-inducible factor 1 alpha; HIF-1alpha; hypoxic tissue;
KW respiratory; cytostatic; vasotropic; virucide; hypoxic condition; cancer;
KW ischaemia; viral infection; drug screening; drug discovery;
KW ligand binding site peptide.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004042361-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US035154.
XX
PR 04-NOV-2002; 2002US-00287670.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Kaelin WG, Livingston DM, Kim T;
XX
DR WPI; 2004-400725/37.
XX
PT New transgenic non-human animal comprising light-generating fusion
PT protein, useful in diagnosing and treating hypoxic conditions, cancer,
PT ischemia and viral infections and in drug screening and discovery.
XX
PS Disclosure; SEQ ID NO 15; 111pp; English.
XX
CC The present invention describes a transgenic non-human animal comprising
CC a recombinant nucleic acid molecule stably integrated into the genome of
CC the animal, where the molecule encodes a light-generating fusion protein
CC comprising a ligand binding site and a light-generating polypeptide
CC moiety. Also described: (1) an isolated cell of the animal; (2) producing
CC a transgenic non-human animal; (3) identifying a compound capable of
CC modifying an activity of hypoxia-inducible factor (HIF) 1 alpha; and (4)
CC detecting hypoxic tissue. The compound has respiratory, cytostatic,
CC vasotropic and virucide activities. The transgenic non-human animal,
CC light-generating fusion protein, agents, kits and compositions are useful
CC in diagnosing and treating hypoxic conditions, cancer, ischaemia and
CC viral infections and in drug screening and discovery. The present
CC sequence represents a HIF-1alpha ligand binding site peptide, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 20 AA;

Query Match 63.5%; Score 101; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 18
AAO23481
ID AAO23481 standard; peptide; 29 AA.
XX
AC AAO23481;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein mutant fragment.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Claim 39; Page 93; 96pp; English.
XX

CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a specific example
CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-
CC related conditions
XX
SQ Sequence 29 AA;

Query Match 63.5%; Score 101; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 19
AAO23499
ID AAO23499 standard; peptide; 29 AA.
XX
AC AAO23499;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region fragment (residues 546-573).
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 6; Fig 19; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a N-TAD region of
CC a murine HIF-1 alpha protein
XX
SQ Sequence 29 AA;

Query Match 63.5%; Score 101; DB 7; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 10 DLDLEMLAPYIPMDDDFQL 28

RESULT 20
AAB49913
ID AAB49913 standard; peptide; 34 AA.
XX
AC AAB49913;
XX
DT 06-MAR-2001 (first entry)
XX
DE Human/murine HIF-1alpha subunit conserved motif #9.
XX
KW Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
KW hypoxia inducible factor-1; cancer; ischaemia.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO200069908-A1.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-GB001826.
XX
PR 12-MAY-1999; 99GB-00011047.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Ratcliffe PJ, Maxwell PH, Pugh CW;
XX
DR WPI; 2001-025006/03.
XX
PT Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
PT subunit interaction modulators for treating ischemia by contacting a VHL
PT protein and an HIF subunit protein with a putative modulator.
XX
PS Claim 14; Page 50; 56pp; English.
XX
CC The present invention describes a novel assay for use in identifying
CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
CC contacting the VHL protein, the HIF-1alpha subunit and the putative
CC modulator under conditions where the former two would normally complex.
CC Modulators of this type are useful in the treatment of cancer and
CC ischaemic conditions such as coronary, cerebral and vascular
CC insufficiency
XX
SQ Sequence 34 AA;

Query Match 63.5%; Score 101; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          12 DLDLEMLAPYIPMDDDFQL 30
               ||||||||||||||||||
Db           8 DLDLEMLAPYIPMDDDFQL 26


RESULT 21
AAE30161
ID   AAE30161 standard; peptide; 34 AA.
XX
AC   AAE30161;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Peptide #1 used to block HIF-1alpha/pVHL interaction.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Example 1; Page 246; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC   interaction. This sequence is used in the invention
XX
SQ   Sequence 34 AA;

  Query Match             63.5%;  Score 101;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 DLDLEMLAPYIPMDDDFQL 30
               ||||||||||||||||||
Db           8 DLDLEMLAPYIPMDDDFQL 26


RESULT 22
AAE30151
ID   AAE30151 standard; peptide; 34 AA.
XX
AC   AAE30151;
XX
DT   24-FEB-2003  (first entry)
XX
DE   HIFalpha subunit antagonist #8.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW   antagonist.
XX
OS   Unidentified.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Disclosure; Page 239; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is HIFalpha subunit antagonist. This
CC   sequence is used in the invention
XX
SQ   Sequence 34 AA;

  Query Match             63.5%;  Score 101;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-07;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 DLDLEMLAPYIPMDDDFQL 30
               ||||||||||||||||||
Db           8 DLDLEMLAPYIPMDDDFQL 26


RESULT 23
AAY94637
ID   AAY94637 standard; protein; 54 AA.
XX
AC   AAY94637;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/531-584.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
```

OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 19; Page 84-85; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 54 AA;

Query Match 63.5%; Score 101; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 26 DLDLEMLAPYIPMDDDFQL 44

RESULT 24
AAO23490
ID AAO23490 standard; peptide; 54 AA.
XX
AC AAO23490;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region fragment (residues 531-584).
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 4; Fig 4; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a N-TAD region of
CC a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 63.5%; Score 101; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 25
AAO23530
ID AAO23530 standard; peptide; 54 AA.
XX
AC AAO23530;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment Q572A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX

PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 11; Fig 27; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 63.5%; Score 101; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 26
AAO23528
ID AAO23528 standard; peptide; 54 AA.
XX
AC AAO23528;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment L573A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 11; Fig 27; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 63.5%; Score 101; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 27
AAO23529
ID AAO23529 standard; peptide; 54 AA.
XX
AC AAO23529;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment QR-A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 11; Fig 27; 96pp; English.

XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 63.5%; Score 101; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 28
AAY94632
ID AAY94632 standard; protein; 116 AA.
XX
AC AAY94632;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/526-641.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 76-77; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 116 AA;

Query Match 63.5%; Score 101; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 29
AAY94633
ID AAY94633 standard; protein; 288 AA.
XX
AC AAY94633;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/526-813.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 77-78; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the

```
CC   molecular probe. The compounds are useful for the regulation of HIF-
CC   1alpha target genes, such as those involved in the regulation of
CC   angiogenesis, erythropoiesis an glycolysis
XX
SQ   Sequence 288 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 288;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db         31 DLDLEMLAPYIPMDDDFQL 49


RESULT 30
AAY94634
ID   AAY94634 standard; protein; 301 AA.
XX
AC   AAY94634;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/526-826.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS   Homo sapiens.
XX
PN   WO200029437-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-SE002053.
XX
PR   13-NOV-1998;   98SE-00003891.
XX
PA   (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI   Berkenstam A,  Poellinger L;
XX
DR   WPI; 2000-399715/34.
XX
PT   Human hypoxia-inducible factor alpha variants for identifying compounds
PT   that modulate its functional domain and regulate genes involved in
PT   angiogenesis, erythropoiesis.
XX
PS   Claim 13; Page 78-79; 87pp; English.
XX
CC   This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC   -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC   multi-step process which includes hypoxia-dependent nuclear import and
CC   activation of the transactivation domain. The HIF-1alpha consists of a
CC   number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC   located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC   nuclear localization sequence located at amino acids 718-584, a
CC   transactivator domain (N-TAD) located between amino acids 531 and 584,
CC   and a second transactivator domain (C-TAD) located between 813 and 826.
CC   The invention relates to isolated variants of HIF-1alpha, such as that
CC   represented by the present sequence. The variants are useful for
CC   identifying compounds capable of modulating the function of a functional
CC   domain of human HIF-1alpha. The method comprises contacting a candidate
CC   compound with a cell expressing a HIF-1alpha variant conjugated to a
CC   molecular probe. The localization of the probe can be detected in the
CC   cell. The Aequeora victoria green fluorescent protein can be used as the
CC   molecular probe. The compounds are useful for the regulation of HIF-
CC   1alpha target genes, such as those involved in the regulation of
CC   angiogenesis, erythropoiesis an glycolysis
XX
SQ   Sequence 301 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db         31 DLDLEMLAPYIPMDDDFQL 49


RESULT 31
AAY94631
ID   AAY94631 standard; protein; 311 AA.
XX
AC   AAY94631;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/331-641.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS   Homo sapiens.
XX
PN   WO200029437-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-SE002053.
XX
PR   13-NOV-1998;   98SE-00003891.
XX
PA   (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI   Berkenstam A,  Poellinger L;
XX
DR   WPI; 2000-399715/34.
XX
PT   Human hypoxia-inducible factor alpha variants for identifying compounds
PT   that modulate its functional domain and regulate genes involved in
PT   angiogenesis, erythropoiesis.
XX
PS   Claim 13; Page 74-75; 87pp; English.
XX
CC   This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC   -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC   multi-step process which includes hypoxia-dependent nuclear import and
CC   activation of the transactivation domain. The HIF-1alpha consists of a
CC   number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC   located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC   nuclear localization sequence located at amino acids 718-584, a
CC   transactivator domain (N-TAD) located between amino acids 531 and 584,
CC   and a second transactivator domain (C-TAD) located between 813 and 826.
CC   The invention relates to isolated variants of HIF-1alpha, such as that
CC   represented by the present sequence. The variants are useful for
CC   identifying compounds capable of modulating the function of a functional
CC   domain of human HIF-1alpha. The method comprises contacting a candidate
CC   compound with a cell expressing a HIF-1alpha variant conjugated to a
CC   molecular probe. The localization of the probe can be detected in the
CC   cell. The Aequeora victoria green fluorescent protein can be used as the
CC   molecular probe. The compounds are useful for the regulation of HIF-
CC   1alpha target genes, such as those involved in the regulation of
CC   angiogenesis, erythropoiesis an glycolysis
XX
SQ   Sequence 311 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        226 DLDLEMLAPYIPMDDDFQL 244
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```
RESULT 32
ADO39389
ID   ADO39389 standard; protein; 409 AA.
XX
AC   ADO39389;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Chimeric transactivator THV fragment #3.
XX
KW   haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW   normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW   inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW   tetracycline resistance; VP16.
XX
OS   Homo sapiens.
XX
PN   US2004018606-A1.
XX
PD   29-JAN-2004.
XX
PF   30-APR-2003; 2003US-00425833.
XX
PR   30-APR-2002; 2002US-0376269P.
XX
PA   (BOHL/) BOHL D.
PA   (HEAR/) HEARD M.
XX
PI   Bohl D,  Heard M;
XX
DR   WPI; 2004-122040/12.
DR   N-PSDB; ADO39384.
XX
PT   New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT   of a transcription factor susceptible to degradation under normoxia
PT   conditions, useful for treating anemia associated with AIDS, cancer and
PT   inflammation.
XX
PS   Disclosure; Fig 6H; 28pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which codes for a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions. Also described are: a chimeric transactivator comprising a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions; an isolated polynucleotide which codes for the chimeric
CC   transactivator (1); a vector comprising the chimeric transactivator
CC   polynucleotide (2); a composition comprising polynucleotide (2) and a
CC   polynucleotide which contains a sequence that codes for a target gene and
CC   a promoter which is regulated by the chimeric transactivator coded; a
CC   method of expressing a target gene in a subject, comprising administering
CC   the composition of (4); a method of increasing the number of red blood
CC   cells in a subject, comprising administering the composition of (4) to
CC   the subject; and a method of increasing the number of blood vessels in
CC   subject, comprising administering the composition of (4) to the subject.
CC   The methods and compositions of the present invention are useful for
CC   treating anaemia associated with AIDS or cancer, anaemia from
CC   inflammatory origin and haemoglobinopathies. This is the amino acid
CC   sequence of a fragment of a chimeric transactivator comprising regions of
CC   the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC   transcription factor gene and VP16.
XX
SQ   Sequence 409 AA;

  Query Match             63.5%;  Score 101;  DB 8;  Length 409;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253
```

```
RESULT 33
AAB68415
ID   AAB68415 standard; protein; 444 AA.
XX
AC   AAB68415;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of tTAk-hH104.
XX
KW   Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
KW   anemia; cancer; ischemia; erythropoietin; immunotherapy;
KW   autoimmune disease; hH104; tTAk.
XX
OS   Synthetic.
XX
PN   WO200136616-A2.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-FR003207.
XX
PR   18-NOV-1999;   99FR-00014513.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Beuzard Y,  Payen E,  Scherman D,  Bettan M;
XX
DR   WPI; 2001-343818/36.
DR   N-PSDB; AAF85323.
XX
PT   New nucleic acid construct for controlling expression of target gene,
PT   useful e.g. for treating cancer, is modulated by exogeneous
PT   pharmaceutical and oxygen partial pressure.
XX
PS   Disclosure; Page 57-58; 60pp; French.
XX
CC   The specification describes a nucleic acid construct bearing a system for
CC   regulating the expression of a gene. The nucleic acid construct comprises
CC   at least one sequence encoding a protein that regulates expression of at
CC   least one gene of interest. The activity of this protein is modulated by
CC   presence/absence of a pharmacological agent and the amount of protein
CC   produced depends on the oxygen partial pressure. The constructs are used
CC   to treat conditions associated with cellular hypoxia, especially anemia,
CC   cancer and ischemia, specifically where the gene of interest encodes
CC   erythropoietin (but many other suitable genes are listed, e.g. those
CC   encoding single-chain antibodies for immunotherapy of infections or
CC   autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
CC   etc.). The present sequence is encoded by the open reading frame of tTAk-
CC   hH104. The sequence contains a human hH104 fragment, inserted into the
CC   BsiWI site of tTAk. The sequence is used to produce constructs of the
CC   invention
XX
SQ   Sequence 444 AA;

  Query Match             63.5%;  Score 101;  DB 4;  Length 444;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        242 DLDLEMLAPYIPMDDDFQL 260
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RESULT 34
ADO39390
ID   ADO39390 standard; protein; 466 AA.
XX
AC   ADO39390;
XX
```

DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #4.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39385.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
PS Disclosure; Fig 6I; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 466 AA;

Query Match 63.5%; Score 101; DB 8; Length 466;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 35
ADO39387
ID ADO39387 standard; protein; 538 AA.
XX
AC ADO39387;

XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #1.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39382.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
PS Disclosure; Fig 6F; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 538 AA;

Query Match 63.5%; Score 101; DB 8; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 36
ABP41474
ID ABP41474 standard; protein; 542 AA.
XX

AC ABP41474;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HNORJ10, SEQ ID NO:2606.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; chromosome 14q21-24.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US018569.
XX
PR 07-JUN-2000; 2000US-0209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABQ54551.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX
PS Claim 11; SEQ ID NO 2606; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 542 AA;

Query Match 63.5%; Score 101; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 272 DLDLEMLAPYIPMDDDFQL 290

RESULT 37
ADO39388
ID ADO39388 standard; protein; 595 AA.
XX
AC ADO39388;
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #2.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39383.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
PS Disclosure; Fig 6G; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 595 AA;

```
  Query Match             63.5%;  Score 101;  DB 8;  Length 595;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        364 DLDLEMLAPYIPMDDDFQL 382


RESULT 38
AAY94630
ID   AAY94630 standard; protein; 613 AA.
XX
AC   AAY94630;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/delta178-390.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS   Homo sapiens.
XX
PN   WO200029437-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-SE002053.
XX
PR   13-NOV-1998;   98SE-00003891.
XX
PA   (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI   Berkenstam A,  Poellinger L;
XX
DR   WPI; 2000-399715/34.
XX
PT   Human hypoxia-inducible factor alpha variants for identifying compounds
PT   that modulate its functional domain and regulate genes involved in
PT   angiogenesis, erythropoiesis.
XX
PS   Claim 13; Page 72-74; 87pp; English.
XX
CC   This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC   -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC   multi-step process which includes hypoxia-dependent nuclear import and
CC   activation of the transactivation domain. The HIF-1alpha consists of a
CC   number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC   located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC   nuclear localization sequence located at amino acids 718-584, a
CC   transactivator domain (N-TAD) located between amino acids 531 and 584,
CC   and a second transactivator domain (C-TAD) located between 813 and 826.
CC   The invention relates to isolated variants of HIF-1alpha, such as that
CC   represented by the present sequence. The variants are useful for
CC   identifying compounds capable of modulating the function of a functional
CC   domain of human HIF-1alpha. The method comprises contacting a candidate
CC   compound with a cell expressing a HIF-1alpha variant conjugated to a
CC   molecular probe. The localization of the probe can be detected in the
CC   cell. The Aequeora victoria green fluorescent protein can be used as the
CC   molecular probe. The compounds are useful for the regulation of HIF-
CC   1alpha target genes, such as those involved in the regulation of
CC   angiogenesis, erythropoiesis an glycolysis
XX
SQ   Sequence 613 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 613;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        343 DLDLEMLAPYIPMDDDFQL 361


RESULT 39
AAU77614
ID   AAU77614 standard; protein; 613 AA.
XX
AC   AAU77614;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Human hypoxia-inducible factor-1 alpha, HIF-1, mutant delta 178-390.
XX
KW   Human; HIF-1; hypoxia-inducible factor-1; rheumatoid arthritis;
KW   transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction;
KW   circulatory disorder; cancer; hypertension; demyelinating disorder;
KW   angiogenesis; sarcoidosis; hepatitis-caused inflammation;
KW   chronic ulceration; neovascularisation; arterial hypervascularisation;
KW   bullous skin disease; vasculitis; dermatomyositis; polymyositis; mutant;
KW   mutein; Y565G.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 177. .178
FT                   /note= "Residues 178-390 of the wild-type HIF-1 have been
FT                   deleted"
XX
PN   WO200212326-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-IB001775.
XX
PR   07-AUG-2000; 2000US-0223480P.
XX
PA   (ASPE-) ASPERA PHARM AB.
XX
PI   Poellinger L,  Pereira T,  Ruas J;
XX
DR   WPI; 2002-257466/30.
XX
PT   New polypeptides comprising hypoxia-inducible factor-1 with alterations
PT   of the transactivation domain, useful treating ischemic conditions, e.g.
PT   brain infarction, heart infarction or circulatory disorder.
XX
PS   Example 5; Page; 80pp; English.
XX
CC   The invention relates to a polypeptide comprising hypoxia-inducible
CC   factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or
CC   C-TAD). Also included are nucleic acids encoding the altered proteins, a
CC   vector comprising the nucleic acid, a host cell transformed with the
CC   vector, methods for producing the protein or its functional fragment or
CC   an isolated degradation box, a method of screening for an agent that
CC   modulates N-TAD function and antagonists, agonists, modulators and HIF-1
CC   peptide fragments useful for modulating HIF-1 function or the function of
CC   proteins that interact with it. The isolated polypeptides and their
CC   fragments with altered residues are useful in methods for treating
CC   diseases. The disease is an ischaemic condition, e.g. brain infarction,
CC   heart infarction or circulatory disorder. The disease may also be cancer,
CC   hypertension, demyelinating disorders, diffuse proliferative
CC   glomerulonephritis, toxoplasmosis caused retinochorioiditis, HIV (human
CC   immunodeficiency virus) caused Tat angiogenesis, HIV-caused Kaposi's
CC   sarcoma, hepatitis-caused inflammation, hepatitis-caused angiogenesis,
CC   chronic ulceration, proliferative retinopathy, retina haemangioblastomas,
CC   neovascularisation, arterial hypervascularisation, sarcoidosis, bullous
CC   skin disease, vasculitis with angiogenesis, dermatomyositis with
CC   angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis,
CC   juvenile osteoarthritis, polyarthritis, aneurysm or atheroma. The present
CC   sequence represents HIF-1 mutant delta 178-390. Note: The present
CC   sequence is not shown in the specification but was created by the indexer
CC   using the information in example 5 and the HIF sequence appearing as
```

```
CC   AAU77602
XX
SQ   Sequence 613 AA;

  Query Match             63.5%;  Score 101;  DB 5;  Length 613;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        343 DLDLEMLAPYIPMDDDFQL 361


RESULT 40
ADO39391
ID   ADO39391 standard; protein; 632 AA.
XX
AC   ADO39391;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Chimeric transactivator THV fragment #5.
XX
KW   haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW   normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW   inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW   tetracycline resistance; VP16.
XX
OS   Homo sapiens.
XX
PN   US2004018606-A1.
XX
PD   29-JAN-2004.
XX
PF   30-APR-2003; 2003US-00425833.
XX
PR   30-APR-2002; 2002US-0376269P.
XX
PA   (BOHL/) BOHL D.
PA   (HEAR/) HEARD M.
XX
PI   Bohl D,  Heard M;
XX
DR   WPI; 2004-122040/12.
DR   N-PSDB; ADO39386.
XX
PT   New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT   of a transcription factor susceptible to degradation under normoxia
PT   conditions, useful for treating anemia associated with AIDS, cancer and
PT   inflammation.
XX
PS   Disclosure; Fig 6J; 28pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which codes for a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions. Also described are: a chimeric transactivator comprising a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions; an isolated polynucleotide which codes for the chimeric
CC   transactivator (1); a vector comprising the chimeric transactivator
CC   polynucleotide (2); a composition comprising polynucleotide (2) and a
CC   polynucleotide which contains a sequence that codes for a target gene and
CC   a promoter which is regulated by the chimeric transactivator coded; a
CC   method of expressing a target gene in a subject, comprising administering
CC   the composition of (4); a method of increasing the number of red blood
CC   cells in a subject, comprising administering the composition of (4) to
CC   the subject; and a method of increasing the number of blood vessels in
CC   subject, comprising administering the composition of (4) to the subject.
CC   The methods and compositions of the present invention are useful for
CC   treating anaemia associated with AIDS or cancer, anaemia from
CC   inflammatory origin and haemoglobinopathies. This is the amino acid
CC   sequence of a fragment of a chimeric transactivator comprising regions of
CC   the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC   transcription factor gene and VP16.
XX
SQ   Sequence 632 AA;

  Query Match             63.5%;  Score 101;  DB 8;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 41
AAY94629
ID   AAY94629 standard; protein; 652 AA.
XX
AC   AAY94629;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/1-652.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS   Homo sapiens.
XX
PN   WO200029437-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-SE002053.
XX
PR   13-NOV-1998;   98SE-00003891.
XX
PA   (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI   Berkenstam A,  Poellinger L;
XX
DR   WPI; 2000-399715/34.
XX
PT   Human hypoxia-inducible factor alpha variants for identifying compounds
PT   that modulate its functional domain and regulate genes involved in
PT   angiogenesis, erythropoiesis.
XX
PS   Claim 15; Page 69-70; 87pp; English.
XX
CC   This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC   -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC   multi-step process which includes hypoxia-dependent nuclear import and
CC   activation of the transactivation domain. The HIF-1alpha consists of a
CC   number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC   located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC   nuclear localization sequence located at amino acids 718-584, a
CC   transactivator domain (N-TAD) located between amino acids 531 and 584,
CC   and a second transactivator domain (C-TAD) located between 813 and 826.
CC   The invention relates to isolated variants of HIF-1alpha, such as that
CC   represented by the present sequence. The variants are useful for
CC   identifying compounds capable of modulating the function of a functional
CC   domain of human HIF-1alpha. The method comprises contacting a candidate
CC   compound with a cell expressing a HIF-1alpha variant conjugated to a
CC   molecular probe. The localization of the probe can be detected in the
CC   cell. The Aequeora victoria green fluorescent protein can be used as the
CC   molecular probe. The compounds are useful for the regulation of HIF-
CC   1alpha target genes, such as those involved in the regulation of
CC   angiogenesis, erythropoiesis an glycolysis
XX
SQ   Sequence 652 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 652;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
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```
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 42
AAY84167
ID   AAY84167 standard; protein; 669 AA.
XX
AC   AAY84167;
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 549-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 669 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        399 DLDLEMLAPYIPMDDDFQL 417


RESULT 43
AAY84166
ID   AAY84166 standard; protein; 697 AA.
XX
AC   AAY84166;
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 422
FT                   /note= "this residue is optionally not Ser, and is
FT                   preferably Gly"
FT   Misc-difference 423
FT                   /note= "this residue is optionally not Thr, and is
FT                   preferably Ala"
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 521-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 697 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        427 DLDLEMLAPYIPMDDDFQL 445


RESULT 44
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```
AAY84173
ID   AAY84173 standard; protein; 701 AA.
XX
AC   AAY84173;
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 426
FT                   /note= "this residue is not Ser, and is preferably Gly"
FT   Misc-difference 427
FT                   /note= "this residue is not Thr, and is preferably Ala"
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 517-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 701 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 701;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        431 DLDLEMLAPYIPMDDDFQL 449


RESULT 45
AAY84172
ID   AAY84172 standard; protein; 710 AA.
XX
AC   AAY84172;
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 435
FT                   /note= "this residue is not Ser, and is preferably Gly"
FT   Misc-difference 436
FT                   /note= "this residue is not Thr, and is preferably Ala"
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 710 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 710;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        440 DLDLEMLAPYIPMDDDFQL 458


RESULT 46
AAY84171
ID   AAY84171 standard; protein; 724 AA.
XX
AC   AAY84171;
```

```
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 449
FT                   /note= "this residue is not Ser, and is preferably Gly"
FT   Misc-difference 450
FT                   /note= "this residue is not Thr, and is preferably Ala"
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 494-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 724 AA;

  Query Match             63.5%;  Score 101;  DB 3;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        454 DLDLEMLAPYIPMDDDFQL 472


RESULT 47
ABR82375
ID   ABR82375 standard; protein; 735 AA.
XX
AC   ABR82375;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hypoxia-inducible factor 1 (HIF-1) alpha variant sequence.
XX
KW   HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW   erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW   tranquillizer; vulnerary; cardiant; cerebroprotective; variant.
XX
OS   Homo sapiens.
XX
PN   WO2003057820-A2.
XX
PD   17-JUL-2003.
XX
PF   04-OCT-2002; 2002WO-US031699.
XX
PR   21-DEC-2001; 2001US-00032361.
XX
PA   (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.
XX
PI   Mcgrath K;
XX
DR   WPI; 2003-645988/61.
XX
PT   Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT   ubiquitination, and activator of vascular endothelial growth factor
PT   transcription useful for treating tissue injuries including wounds,
PT   surgical incisions.
XX
PS   Disclosure; Page 5-6; 37pp; English.
XX
CC   The invention relates to peptide inhibitors of hypoxia-inducible factor
CC   (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC   transcription of erythropoietin (EPO), vascular endothelial growth factor
CC   (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC   for treating tissue injuries including wounds, surgical incisions,
CC   chronic wounds, heart disease and stroke. The present sequence represents
CC   a HIF-1 alpha variant sequence
XX
SQ   Sequence 735 AA;

  Query Match             63.5%;  Score 101;  DB 6;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 48
ADN75066
ID   ADN75066 standard; protein; 735 AA.
XX
AC   ADN75066;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human hypoxia-inducible factor 1 alpha #2.
XX
KW   human; antisense therapy; hypoxia-inducible factor 1 alpha;
KW   hyperproliferative disorder.
XX
OS   Homo sapiens.
XX
PN   US2004101858-A1.
XX
PD   27-MAY-2004.
XX
PF   23-NOV-2002; 2002US-00304126.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (ISIS-) ISIS PHARM INC.
```

XX
PI Ward DT, Dobie KW;
XX
DR WPI; 2004-399686/37.
DR N-PSDB; ADN74945.
XX
PT New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding hypoxia-inducible factor 1 alpha, useful for treating diseases
PT associated with hypoxia-inducible factor 1 alpha, e.g. hyperproliferative
PT disorders.
XX
PS Disclosure; Page 57-59; 80pp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to, and
CC which specifically hybridise with, and inhibit expression of, a nucleic
CC acid molecule encoding hypoxia-inducible factor 1 alpha. The antisense
CC oligonucleotides are useful for treating a disease or condition
CC associated with hypoxia-inducible factor 1 alpha, such as a
CC hyperproliferative disorder. They are also useful in research and
CC diagnostics for modulating the expression of hypoxia-inducible factor 1
CC alpha. The present sequence represents human hypoxia-inducible factor 1
CC alpha #2.
XX
SQ Sequence 735 AA;

Query Match 63.5%; Score 101; DB 8; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 49
AAY84170
ID AAY84170 standard; protein; 749 AA.
XX
AC AAY84170;
XX
DT 03-JUL-2000 (first entry)
XX
DE A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 474
FT /note= "this residue is not Ser, and is preferably Gly"
FT Misc-difference 475
FT /note= "this residue is not Thr, and is preferably Ala"
XX
PN WO200010578-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019416.
XX
PR 25-AUG-1998; 98US-00148547.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Semenza GL;
XX
DR WPI; 2000-246493/21.
XX
PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.
XX
PS Claim 1; Page; 96pp; English.
XX
CC The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 469-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They is also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 749 AA;

Query Match 63.5%; Score 101; DB 3; Length 749;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 479 DLDLEMLAPYIPMDDDFQL 497

RESULT 50
AAY94635
ID AAY94635 standard; protein; 756 AA.
XX
AC AAY94635;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/71-826.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 20; Page 79-82; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal

CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 756 AA;

Query Match 63.5%; Score 101; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 486 DLDLEMLAPYIPMDDDFQL 504

Search completed: February 9, 2005, 06:05:43
Job time : 168.175 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 79.4737 Seconds
(without alignments)
193.301 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 159
Sequence: 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	65.4	766	1	HIFA_ONCMY	Q98sw2 oncorhynchu
2	103	64.8	777	2	Q6EHI4	Q6ehi4 brachydanio
3	102	64.2	774	2	Q6STN7	Q6stn7 ctenopharyn
4	101	63.5	786	2	Q6SLL1	Q6sll1 canis famil
5	101	63.5	802	2	Q6PI54	Q6pi54 xenopus lae
6	101	63.5	805	1	HIFA_XENLA	Q9i8a9 xenopus lae
7	101	63.5	811	1	HIFA_CHICK	Q9yib9 gallus gall
8	101	63.5	819	2	Q7YSE5	Q7yse5 oryctolagus
9	101	63.5	821	2	Q64F54	Q64f54 spermophilu
10	101	63.5	823	1	HIFA_BOVIN	Q9xta5 bos taurus
11	101	63.5	823	2	Q6IV47	Q6iv47 bos mutus g
12	101	63.5	824	2	Q6H8T3	Q6h8t3 spalax juda
13	101	63.5	825	1	HIFA_RAT	O35800 rattus norv
14	101	63.5	826	1	HIFA_HUMAN	Q16665 homo sapien
15	101	63.5	836	1	HIFA_MOUSE	Q61221 mus musculu
16	87	54.7	630	2	Q9QX54	Q9qx54 mus musculu
17	87	54.7	632	2	Q8WXA1	Q8wxa1 homo sapien
18	87	54.7	643	2	Q6STN6	Q6stn6 ctenopharyn
19	87	54.7	648	2	Q9HAI2	Q9hai2 homo sapien
20	87	54.7	662	2	Q9Z2I5	Q9z2i5 mus musculu
21	87	54.7	667	2	Q9Y2N7	Q9y2n7 homo sapien
22	87	54.7	669	2	Q66K72	Q66k72 homo sapien
23	86	54.1	571	2	Q7T2E4	Q7t2e4 brachydanio
24	86	54.1	626	2	Q6EGR9	Q6egr9 brachydanio
25	84.5	53.1	662	2	Q9JHS2	Q9jhs2 rattus norv
26	82.5	51.9	859	2	Q6GQ12	Q6gq12 xenopus lae
27	80.5	50.6	835	2	Q696W2	Q696w2 ctenopharyn
28	80.5	50.6	862	2	Q6GL61	Q6gl61 xenopus tro
29	80.5	50.6	862	2	Q6GP97	Q6gp97 xenopus lae
30	80.5	50.6	873	2	Q8QGM4	Q8qgm4 fundulus he
31	80	50.3	632	2	Q96K34	Q96k34 homo sapien
32	76.5	48.1	163	2	Q6RYD1	Q6ryd1 sus scrofa
33	76.5	48.1	164	2	Q6RYD0	Q6ryd0 ovis aries
34	76.5	48.1	867	2	Q9W7C6	Q9w7c6 gallus gall
35	76.5	48.1	870	1	PAS1_HUMAN	Q99814 homo sapien
36	76.5	48.1	870	2	Q9XTA4	Q9xta4 bos taurus
37	76.5	48.1	870	2	Q9PTB3	Q9ptb3 coturnix co
38	76.5	48.1	874	1	PAS1_MOUSE	P97481 mus musculu
39	76.5	48.1	874	1	PAS1_RAT	Q9jhs1 rattus norv
40	76.5	48.1	874	2	Q6PEU2	Q6peu2 mus musculu
41	65	40.9	235	2	Q8QGI5	Q8qgi5 fundulus he
42	64.5	40.6	72	2	Q6GXZ1	Q6gxz1 human immun
43	62.5	39.3	71	2	Q71939	Q71939 human immun
44	62.5	39.3	71	2	Q71945	Q71945 human immun
45	62.5	39.3	99	2	Q8UT76	Q8ut76 human immun
46	62.5	39.3	101	2	Q90CH6	Q90ch6 human immun
47	62.5	39.3	101	2	Q90CY2	Q90cy2 human immun
48	62	39.0	86	2	Q8ADC2	Q8adc2 human immun
49	61.5	38.7	72	2	Q69628	Q69628 human immun
50	61	38.4	72	2	P88699	P88699 human immun
51	60.5	38.1	420	2	Q9FJJ4	Q9fjj4 arabidopsis
52	59.5	37.4	101	2	Q8QDF8	Q8qdf8 human immun
53	59.5	37.4	101	2	Q994G0	Q994g0 human immun
54	59	37.1	86	2	Q8ADL8	Q8adl8 human immun
55	59	37.1	99	2	Q902T6	Q902t6 human immun
56	59	37.1	101	2	Q8Q7Z3	Q8q7z3 human immun
57	59	37.1	101	2	Q7ZJE0	Q7zje0 human immun
58	59	37.1	685	2	Q9RTU7	Q9rtu7 deinococcus
59	59	37.1	881	1	DX54_HUMAN	Q8tdd1 homo sapien
60	58.5	36.8	72	2	P90127	P90127 human immun
61	58.5	36.8	72	2	Q6GXZ2	Q6gxz2 human immun
62	58.5	36.8	72	2	Q6GXZ3	Q6gxz3 human immun
63	58.5	36.8	72	2	Q6GXZ4	Q6gxz4 human immun
64	58.5	36.8	72	2	Q6GXZ6	Q6gxz6 human immun
65	58.5	36.8	101	2	O71264	O71264 human immun

ALIGNMENTS

RESULT 1
HIFA_ONCMY
ID HIFA_ONCMY STANDARD; PRT; 766 AA.
AC Q98SW2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282949; PubMed=11278461; DOI=10.1074/jbc.M009057200;
RA Soitamo A.J., Rabergh C.M.I., Gassmann M., Sistonen L., Nikinmaa M.;
RT "Characterization of a hypoxia-inducible factor (HIF-1 alpha) from
RT rainbow trout: accumulation of protein occurs at normal venous oxygen
RT tension.";
RL J. Biol. Chem. 276:19699-19705(2001).
CC -!- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC gene promoters. Activation requires recruitment of transcriptional
CC coactivators (By similarity).
CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

```
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ----------------------------------------------------------------------
DR   EMBL; AF304864; AAK30364.1; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; DNA-binding; Nuclear protein; Repeat;
KW   Transcription regulation.
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       82    159       PAS 1.
FT   DOMAIN      230    300       PAS 2.
FT   DOMAIN      304    347       PAC.
FT   DOMAIN      368    373       Poly-Glu.
SQ   SEQUENCE   766 AA;  85049 MW;  FC25A4984104DA5B CRC64;

  Query Match             65.4%;  Score 104;  DB 1;  Length 766;
  Best Local Similarity   87.0%;  Pred. No. 4.4e-06;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 QRRRDLDLEMLAPYIPMDDDFQL 30
              |   ||||||||||||||||||||
Db        547 QAMEDLDLEMLAPYIPMDDDFQL 569


RESULT 2
Q6EHI4
ID   Q6EHI4      PRELIMINARY;      PRT;   777 AA.
AC   Q6EHI4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypoxia inducible factor 1 alpha.
GN   Name=hif1a;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang C.-R., Tsai Y.-C., Young H.-W., Wang W.-D., Hu C.-H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY326951; AAQ91619.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   777 AA;  85897 MW;  A9AFE2D2732C7A33 CRC64;

  Query Match             64.8%;  Score 103;  DB 2;  Length 777;
  Best Local Similarity   87.0%;  Pred. No. 6.3e-06;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 QRRRDLDLEMLAPYIPMDDDFQL 30
              |   ||||||||||||||||||||
Db        545 QPMEDLDLEMLAPYIPMDDDFQL 567


RESULT 3
Q6STN7
ID   Q6STN7      PRELIMINARY;      PRT;   774 AA.
AC   Q6STN7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia-inducible factor-1alpha.
GN   Name=hif-1alpha;
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY450269; AAR95697.2; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   774 AA;  85741 MW;  15BD0B2F90C611C6 CRC64;

  Query Match             64.2%;  Score 102;  DB 2;  Length 774;
  Best Local Similarity   87.0%;  Pred. No. 8.7e-06;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 QRRRDLDLEMLAPYIPMDDDFQL 30
              |   ||||||||||||||||||||
Db        543 QAIEDLDLEMLAPYIPMDDDFQL 565


RESULT 4
Q6SLL1
ID   Q6SLL1      PRELIMINARY;      PRT;   786 AA.
AC   Q6SLL1;
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha subunit (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Spee B., Penning L.C., Rothuizen J.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY455802; AAR19225.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
FT   NON_TER       1      1
FT   NON_TER     786    786
SQ   SEQUENCE   786 AA;  88015 MW;  C37A27C25C343CDC CRC64;

  Query Match             63.5%;  Score 101;  DB 2;  Length 786;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        536 DLDLEMLAPYIPMDDDFQL 554


RESULT 5
Q6PI54
ID   Q6PI54      PRELIMINARY;      PRT;   802 AA.
AC   Q6PI54;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hif1a-prov protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC043769; AAH43769.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   802 AA;  90177 MW;  30A571277A9A5B1F CRC64;

  Query Match             63.5%;  Score 101;  DB 2;  Length 802;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        550 DLDLEMLAPYIPMDDDFQL 568


RESULT 6
HIFA_XENLA
ID   HIFA_XENLA      STANDARD;      PRT;   805 AA.
AC   Q9I8A9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=HIF1A;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kietzmann T.;
RT   "Cloning and expression of the Xenopus laevis hypoxia inducible factor
RT   1 alpha homologue.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Binds to core DNA sequence 5'-
```

```
CC       [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC       gene promoters. Activation requires recruitment of transcriptional
CC       coactivators (By similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277829; CAB96628.1; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; FALSE_NEG.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; DNA-binding; Nuclear protein; Repeat;
KW   Transcription regulation.
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       85    157       PAS 1.
FT   DOMAIN      229    300       PAS 2.
FT   DOMAIN      303    346       PAC.
SQ   SEQUENCE   805 AA;  90964 MW;  BABFA0BD6B44FF3B CRC64;

  Query Match             63.5%;  Score 101;  DB 1;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        552 DLDLEMLAPYIPMDDDFQL 570


RESULT 7
HIFA_CHICK
ID   HIFA_CHICK     STANDARD;      PRT;   811 AA.
AC   Q9YIB9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=HIF1A;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Takahashi T.;
RT   "Molecular cloning and expression of an avian cDNA for hypoxia-
RT   inducible factor-1 alpha in embryonic ventricular myocytes.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC       [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC       gene promoters. Activation requires recruitment of transcriptional
CC       coactivators (By similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB013746; BAA34234.2; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; DNA-binding; Nuclear protein; Repeat;
KW   Transcription regulation.
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       80    157       PAS 1.
FT   DOMAIN      228    298       PAS 2.
FT   DOMAIN      302    345       PAC.
FT   DOMAIN      401    587       ODD.
FT   DOMAIN      529    573       NTAD.
FT   DOMAIN      576    785       ID.
FT   DOMAIN      703    706       Nuclear localization signal (Potential).
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DOMAIN      771    811       CTAD.
FT   DOMAIN      583    588       Poly-Ser.
SQ   SEQUENCE   811 AA;  90542 MW;  D14CD9FC98F064CB CRC64;

  Query Match             63.5%;  Score 101;  DB 1;  Length 811;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        554 DLDLEMLAPYIPMDDDFQL 572


RESULT 8
Q7YSE5
ID   Q7YSE5      PRELIMINARY;      PRT;   819 AA.
AC   Q7YSE5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia inducible factor 1 alpha subunit.
OS   Oryctolagus cuniculus (Rabbit).
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```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clausen I., Kietz S., Fischer B.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY273790; AAP43517.1; -.
DR   HSSP; Q16665; 1H2K.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   819 AA;  91284 MW;  E11B4FBF7D4F6C7C CRC64;

  Query Match             63.5%;  Score 101;  DB 2;  Length 819;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 9
Q64F54
ID   Q64F54      PRELIMINARY;      PRT;   821 AA.
AC   Q64F54;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha subunit.
OS   Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Spermophilus.
OX   NCBI_TaxID=43179;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Morin P. Jr., Storey K.B.;
RT   "Cloning and expression of HIF-1 from the hibernating ground squirrel,
RT   Spermophilus tridecemlineatus.";
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY713478; AAU14021.1; -.
SQ   SEQUENCE   821 AA;  92028 MW;  4C96BD0355CCCE06 CRC64;

  Query Match             63.5%;  Score 101;  DB 2;  Length 821;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 10
HIFA_BOVIN
ID   HIFA_BOVIN     STANDARD;      PRT;   823 AA.
AC   Q9XTA5;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=HIF1A;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Artery;
RX   MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA   Hara S., Kobayashi C., Imura N.;
RT   "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-
RT   1alpha and -2alpha of bovine arterial endothelial cells.";
RL   Biochim. Biophys. Acta 1445:237-243(1999).
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Under hypoxic conditions activates
CC       the transcription of over 40 genes, including, erythropoietin,
CC       glucose transporters, glycolytic enzymes, vascular endothelial
CC       growth factor, and other genes whose protein products increase
CC       oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC       Plays an essential role in embryonic vascularization, tumor
CC       angiogenesis and pathophysiology of ischemic disease. Binds to
CC       core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC       element (HRE) of target gene promoters. Activation requires
CC       recruitment of transcriptional coactivators such as CREBPB and
CC       EP300. Activity is enhanced by interaction with both, NCOA1 or
CC       NCOA2. Interaction with redox regulatory protein APEX seems to
CC       activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC       CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-564 in the
CC       oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC       EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-564.
CC       The hydroxylated prolines promote interaction with VHL, initiating
CC       rapid ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-800 by HIF1AN, thus
CC       abrogating interaction with CREBBP and EP300 and preventing
CC       transcriptional activation (By similarity).
CC   -!- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC       nitrosylation in vitro, however not all thiol groups seem to be
CC       nitrolysated in vivo (By similarity).
CC   -!- PTM: Acetylation of Lys-532 by ARD1 increases interaction with VHL
CC       and stimulates subsequent proteasomal degradation (By similarity).
CC   -!- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB018398; BAA78675.1; -.
DR   HSSP; Q16665; 1L8C.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
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DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
KW   Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       85    158       PAS 1.
FT   DOMAIN      228    298       PAS 2.
FT   DOMAIN      302    345       PAC.
FT   DOMAIN      401    600       ODD.
FT   DOMAIN      531    575       NTAD.
FT   DOMAIN      576    782       ID.
FT   DOMAIN      783    823       CTAD.
FT   DOMAIN      715    718       Nuclear localization signal (Potential).
FT   MOD_RES      90     90       S-nitrosocysteine (Potential).
FT   MOD_RES     139    139       S-nitrosocysteine (Potential).
FT   MOD_RES     173    173       S-nitrosocysteine (Potential).
FT   MOD_RES     194    194       S-nitrosocysteine (Potential).
FT   MOD_RES     210    210       S-nitrosocysteine (Potential).
FT   MOD_RES     219    219       S-nitrosocysteine (Potential).
FT   MOD_RES     224    224       S-nitrosocysteine (Potential).
FT   MOD_RES     255    255       S-nitrosocysteine (Potential).
FT   MOD_RES     334    334       S-nitrosocysteine (Potential).
FT   MOD_RES     337    337       S-nitrosocysteine (Potential).
FT   MOD_RES     359    359       S-nitrosocysteine (Potential).
FT   MOD_RES     402    402       Hydroxyproline (By similarity).
FT   MOD_RES     520    520       S-nitrosocysteine (Potential).
FT   MOD_RES     532    532       N6-acetyllysine (By similarity).
FT   MOD_RES     564    564       Hydroxyproline (By similarity).
FT   MOD_RES     755    755       S-nitrosocysteine (Potential).
FT   MOD_RES     777    777       S-nitrosocysteine (Potential).
FT   MOD_RES     797    797       S-nitrosocysteine (Potential).
FT   MOD_RES     800    800       3-hydroxyasparagine (By similarity).
SQ   SEQUENCE   823 AA;  92127 MW;  12674E467A61B1A1 CRC64;

  Query Match             63.5%;  Score 101;  DB 1;  Length 823;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 11
Q6IV47
ID   Q6IV47      PRELIMINARY;      PRT;   823 AA.
AC   Q6IV47;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia inducible factor-1a.
GN   Name=HIF-1A;
OS   Bos mutus grunniens (Yak).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=30521;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dolt K.S., Qadar Pasha M.A.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY621118; AAT39520.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   823 AA;  92128 MW;  A6E388E4FEA15705 CRC64;

  Query Match             63.5%;  Score 101;  DB 2;  Length 823;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 12
Q6H8T3
ID   Q6H8T3      PRELIMINARY;      PRT;   824 AA.
AC   Q6H8T3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia inducible factor 1 alpha.
GN   Name=hif-1a;
OS   Spalax judaei (Blind subterranean mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC   Spalax.
OX   NCBI_TaxID=134510;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Shams I., Avivi A., Nevo E.;
RT   "Hypoxic stress tolerance of the subterranean mole rat: Expression of
RT   erythropoietin and hypoxia-inducible factor-1a.";
RL   Nucleic Acids Res. 0:0-0(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=15210955; DOI=10.1073/pnas.0403540101;
RA   Shams I., Avivi A., Eviatar N.;
RT   "Hypoxic stress tolerance of the blind subterranean mole rat:
RT   expression of erythropoietin and hypoxia-inducible factor 1 alpha.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9698-9703(2004).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AJ715791; CAG29396.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
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DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   824 AA;  92161 MW;  33A1DDC3593CBFFF CRC64;

  Query Match           63.5%;  Score 101;  DB 2;  Length 824;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 13
HIFA_RAT
ID   HIFA_RAT      STANDARD;      PRT;   825 AA.
AC   O35800; Q9WTU9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=Hif1a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Hepatocytes;
RX   MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA   Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;
RT   "Perivenous expression of the mRNA of the three hypoxia-inducible
RT   factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL   Biochem. J. 354:531-537(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX   MEDLINE=21417706; PubMed=11526200;
RA   Zou A.-P., Yang Z.-Z., Li P.-L., Cowley A.W. Jr.;
RT   "Oxygen-dependent expression of hypoxia-inducible factor-1alpha in
RT   renal medullary cells of rats.";
RL   Physiol. Genomics 6:159-168(2001).
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Under hypoxic conditions activates
CC       the transcription of over 40 genes, including, erythropoietin,
CC       glucose transporters, glycolytic enzymes, vascular endothelial
CC       growth factor, and other genes whose protein products increase
CC       oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC       Plays an essential role in embryonic vascularization, tumor
CC       angiogenesis and pathophysiology of ischemic disease. Binds to
CC       core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC       element (HRE) of target gene promoters. Activation requires
CC       recruitment of transcriptional coactivators such as CREBPB and
CC       EP300. Activity is enhanced by interaction with both, NCOA1 or
CC       NCOA2. Interaction with redox regulatory protein APEX seems to
CC       activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC       CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is
CC       seen in the renal medulla than in the cortex. Expressed also in
CC       the perivenous zone of the liver.
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the
CC       oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC       EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563.
CC       The hydroxylated prolines promote interaction with VHL, initiating
CC       rapid ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus
CC       abrogating interaction with CREBBP and EP300 and preventing
CC       transcriptional activation (By similarity).
CC   -!- PTM: S-nitrosylated. All free thiol groups are subjected to S-
CC       nitrosylation in vitro, however not all thiol groups seem to be
CC       nitrolysated in vivo (By similarity).
CC   -!- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL
CC       and stimulates subsequent proteasomal degradation (By similarity).
CC   -!- PTM: Phosphorylation is required for DNA binding (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y09507; CAA70701.1; -.
DR   EMBL; AF057308; AAD24413.1; -.
DR   HSSP; Q16665; 1L8C.
DR   TRANSFAC; T05461; -.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
KW   Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       85    158       PAS 1.
FT   DOMAIN      228    298       PAS 2.
FT   DOMAIN      302    345       PAC.
FT   DOMAIN      401    602       ODD.
FT   DOMAIN      530    574       NTAD.
FT   DOMAIN      575    784       ID.
FT   DOMAIN      717    720       Nuclear localization signal (Potential).
FT   DOMAIN      785    825       CTAD.
FT   MOD_RES      90     90       S-nitrosocysteine (Potential).
FT   MOD_RES     139    139       S-nitrosocysteine (Potential).
FT   MOD_RES     173    173       S-nitrosocysteine (Potential).
FT   MOD_RES     194    194       S-nitrosocysteine (Potential).
FT   MOD_RES     210    210       S-nitrosocysteine (Potential).
FT   MOD_RES     219    219       S-nitrosocysteine (Potential).
FT   MOD_RES     224    224       S-nitrosocysteine (Potential).
FT   MOD_RES     255    255       S-nitrosocysteine (Potential).
FT   MOD_RES     334    334       S-nitrosocysteine (Potential).
FT   MOD_RES     337    337       S-nitrosocysteine (Potential).
FT   MOD_RES     385    385       S-nitrosocysteine (Potential).
FT   MOD_RES     402    402       Hydroxyproline (By similarity).
FT   MOD_RES     519    519       S-nitrosocysteine (Potential).
FT   MOD_RES     531    531       N6-acetyllysine (By similarity).
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FT   MOD_RES     563    563       Hydroxyproline (By similarity).
FT   MOD_RES     779    779       S-nitrosocysteine (Potential).
FT   MOD_RES     799    799       S-nitrosocysteine (Potential).
FT   MOD_RES     802    802       3-hydroxyasparagine (By similarity).
FT   CONFLICT     12     12       K -> NR (in Ref. 2).
FT   CONFLICT     74     74       D -> G (in Ref. 2).
FT   CONFLICT     96     96       P -> L (in Ref. 2).
FT   CONFLICT    329    329       D -> N (in Ref. 2).
FT   CONFLICT    613    619       ATATTAT -> TATA (in Ref. 2).
FT   CONFLICT    708    708       R -> K (in Ref. 2).
SQ   SEQUENCE   825 AA;  92319 MW;  C4109A57F38667E9 CRC64;

  Query Match             63.5%;  Score 101;  DB 1;  Length 825;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              |||||||||||||||||||
Db        555 DLDLEMLAPYIPMDDDFQL 573


RESULT 14
HIFA_HUMAN
ID   HIFA_HUMAN     STANDARD;      PRT;   826 AA.
AC   Q16665; Q96PT9; Q9UPB1;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE   interacting protein) (Member of PAS protein 1) (MOP1).
GN   Name=HIF1A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
RX   MEDLINE=95296340; PubMed=7539918;
RA   Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;
RT   "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
RT   heterodimer regulated by cellular O2 tension.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hepatoma;
RX   MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA   Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA   Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT   "Characterization of a subset of the basic-helix-loop-helix-PAS
RT   superfamily that interacts with components of the dioxin signaling
RT   pathway.";
RL   J. Biol. Chem. 272:8581-8593(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99000835; PubMed=9782081; DOI=10.1006/geno.1998.5416;
RA   Iyer N.V., Leung S.W., Semenza G.L.;
RT   "The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
RT   evolutionary conservation.";
RL   Genomics 52:159-165(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Rupert J.L., Hochachka P.W.;
RT   "HIF1a sequence in the Quechua, a high altitude population.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Glial tumor;
RA   Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Liver;
RA   Tanaka S., Sugimachi K.;
RT   "Hypoxia-inducible factor-1 alpha variant isolated from human liver
RT   tissue.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Choriocarcinoma, and Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   TRANSACTIVATION DOMAINS NTAD AND CTAD.
RX   MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;
RA   Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;
RT   "Transactivation and inhibitory domains of hypoxia-inducible factor
RT   1alpha. Modulation of transcriptional activity by oxygen tension.";
RL   J. Biol. Chem. 272:19253-19260(1997).
RN   [9]
RP   SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.
RX   MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;
RA   Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,
RA   Poellinger L.;
RT   "Signal transduction in hypoxic cells: inducible nuclear translocation
RT   and recruitment of the CBP/p300 coactivator by the hypoxia-inducible
RT   factor-1alpha.";
RL   EMBO J. 17:6573-6586(1998).
RN   [10]
RP   OXYGEN-DEPENDENT DEGRADATION DOMAIN.
RX   MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;
RA   Huang L.E., Gu J., Schau M., Bunn H.F.;
RT   "Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-
RT   dependent degradation domain via the ubiquitin-proteasome pathway.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992(1998).
RN   [11]
RP   TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP   MUTAGENESIS OF CYS-800.
RX   MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA   Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA   Poellinger L., Fujii-Kuriyama Y.;
RT   "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT   in response to hypoxia: their stabilization and redox signal-induced
RT   interaction with CBP/p300.";
RL   EMBO J. 18:1905-1914(1999).
RN   [12]
RP   INTERACTION WITH NCOA1; NCOA2 AND APEX.
RX   MEDLINE=20063199; PubMed=10594042;
RA   Carrero P., Okamoto K., Coumailleau P., O'Brien S., Tanaka H.,
RA   Poellinger L.;
RT   "Redox-regulated recruitment of the transcriptional coactivators CREB-
RT   binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";
RL   Mol. Cell. Biol. 20:402-415(2000).
RN   [13]
RP   MUTAGENESIS OF SER-551 AND THR-552.
RX   MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;
RA   Sutter C.H., Laughner E., Semenza G.L.;
RT   "Hypoxia-inducible factor 1alpha protein expression is controlled by
```

RT oxygen-regulated ubiquitination that is disrupted by deletions and
RT missense mutations.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753(2000).
RN [14]
RP UBIQUITINATION.
RX MEDLINE=21214630; PubMed=11292861; DOI=10.1126/science.1059796;
RA Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
RA Gaskell S.J., von Kriegsheim A., Hebestreit H.F., Mukherji M.,
RA Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.;
RT "Targeting of HIF-alpha to the von Hippel-Lindau ubiquitylation
RT complex by O2-regulated prolyl hydroxylation.";
RL Science 292:468-472(2001).
RN [15]
RP S-NITROSYLATION.
RX MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793(02)03887-5;
RA Sumbayev V.V., Budde A., Zhou J., Bruene B.;
RT "HIF-1 alpha protein as a target for S-nitrosation.";
RL FEBS Lett. 535:106-112(2003).
RN [16]
RP ACETYLATION OF LYS-532.
RX MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674(02)01085-1;
RA Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
RA Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
RT "Regulation and destabilization of HIF-1alpha by ARD1-mediated
RT acetylation.";
RL Cell 111:709-720(2002).
RN [17]
RP HYDROXYLATION OF ASN-803.
RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA Bruick R.K.;
RT "FIH-1 is an asparaginyl hydroxylase enzyme that regulates the
RT transcriptional activity of hypoxia-inducible factor.";
RL Genes Dev. 16:1466-1471(2002).
RN [18]
RP HYDROXYLATION OF PRO-402 AND PRO-564.
RX MEDLINE=21558830; PubMed=11598268; DOI=10.1126/science.1066373;
RA Bruick R.K., McKnight S.L.;
RT "A conserved family of prolyl-4-hydroxylases that modify HIF.";
RL Science 294:1337-1340(2001).
RN [19]
RP REVIEW.
RX MEDLINE=20407247; PubMed=10950862;
RA Semenza G.L.;
RT "HIF-1 and human disease: one highly involved factor.";
RL Genes Dev. 14:1983-1991(2000).
RN [20]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=20539371; PubMed=11089639;
RA Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
RA Michiels C.;
RT "A model for the complex between the hypoxia-inducible factor-1 (HIF-
RT 1) and its consensus DNA sequence.";
RL J. Biomol. Struct. Dyn. 18:169-179(2000).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
RP HIF1AN.
RX MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
RA Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.F.,
RA Schlemminger I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
RT "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
RT mechanism of oxidative modification of HIF-1 alpha.";
RL J. Biol. Chem. 278:1802-1806(2003).
RN [22]
RP STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
RX MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
RA Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
RA Wagner G., Eck M.J.;
RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
RT factor-1 alpha.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372(2002).
RN [23]
RP STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.
RX MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
RA Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
RA Wright P.E.;
RT "Structural basis for Hif-1 alpha /CBP recognition in the cellular

Query Match 63.5%; Score 101; DB 1; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 15
HIFA_MOUSE
ID HIFA_MOUSE STANDARD; PRT; 836 AA.
AC Q61221; O08741; O08993; Q61664; Q61665; Q8C681; Q8CC19; Q8CCB6;
AC Q8R385; Q9CYA8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE interacting protein).
GN Name=Hif1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Hepatocytes;
RX MEDLINE=96355491; PubMed=8702901; DOI=10.1074/jbc.271.35.21262;
RA Li H., Ko H.P., Whitlock J.P. Jr.;
RT "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
RT Roles of Arnt and HIF1alpha.";
RL J. Biol. Chem. 271:21262-21267(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=129/SvJ;
RX MEDLINE=98034461; PubMed=9368100;
RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
RA Bradfield C.A.;
RT "Molecular characterization of the murine Hif-1 alpha locus.";
RL Gene Expr. 6:287-299(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=129/Sv;
RX MEDLINE=97354184; PubMed=9210478;
RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
RA Gassmann M.;
RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
RT organization, expression and characterization of an alternative first
RT exon and 5' flanking sequence.";
RL Eur. J. Biochem. 246:155-165(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Colon, Diencephalon, Embryo, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 13-822 FROM N.A. (ISOFORM 2).
RC TISSUE=Hepatocytes;
RX MEDLINE=96254028; PubMed=8660378; DOI=10.1006/bbrc.1996.0845;
RA Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.;
RT "Nucleotide sequence, chromosomal assignment and mRNA expression of
RT mouse hypoxia-inducible factor-1 alpha.";
RL Biochem. Biophys. Res. Commun. 223:54-59(1996).
RN [7]
RP SEQUENCE OF 22-85 FROM N.A.
RC TISSUE=Hepatocytes;
RA O'Rourke J.F.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Under hypoxic conditions activates
CC the transcription of over 40 genes, including, erythropoietin,
CC glucose transporters, glycolytic enzymes, vascular endothelial
CC growth factor, and other genes whose protein products increase
CC oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC Plays an essential role in embryonic vascularization, tumor
CC angiogenesis and pathophysiology of ischemic disease. Binds to
CC core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC element (HRE) of target gene promoters. Activation requires
CC recruitment of transcriptional coactivators such as CREBPB and
CC EP300. Activity is enhanced by interaction with both, NCOA1 or
CC NCOA2. Interaction with redox regulatory protein APEX seems to
CC activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC similarity).
CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q61221-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q61221-2; Sequence=VSP_007739;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- DOMAIN: Contains two independent C-terminal transactivation
CC domains, NTAD and CTAD, which function synergistically. Their
CC transcriptional activity is repressed by an intervening inhibitory
CC domain (ID) (By similarity).
CC -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-577 in the
CC oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-577.
CC The hydroxylated prolines promote interaction with VHL, initiating
CC rapid ubiquitination and subsequent proteasomal degradation. Under
CC hypoxia, proline hydroxylation is impaired and ubiquitination is
CC attenuated, resulting in stabilization (By similarity).
CC -!- PTM: In normoxia, is hydroxylated on Asn-813 by HIF1AN, thus
CC abrogating interaction with CREBBP and EP300 and preventing
CC transcriptional activation (By similarity).
CC -!- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC nitrosylation in vitro, however not all thiol groups seem to be
CC nitrolysated in vivo (By similarity).
CC -!- PTM: Acetylation of Lys-545 by ARD1 increases interaction with VHL
CC and stimulates subsequent proteasomal degradation (By similarity).
CC -!- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC ----------

CC ----------
DR EMBL; U59496; AAC52730.1; -.
DR EMBL; AF003695; AAC53455.1; -.
DR EMBL; Y09085; CAA70306.1; -.
DR EMBL; Y13656; CAA70306.1; JOINED.
DR EMBL; Y09085; CAA70305.1; -.
DR EMBL; AF004155; AAC53461.1; -.
DR EMBL; AF004141; AAC53461.1; JOINED.
DR EMBL; AF004142; AAC53461.1; JOINED.
DR EMBL; AF004143; AAC53461.1; JOINED.
DR EMBL; AF004144; AAC53461.1; JOINED.
DR EMBL; AF004145; AAC53461.1; JOINED.
DR EMBL; AF004146; AAC53461.1; JOINED.
DR EMBL; AF004147; AAC53461.1; JOINED.
DR EMBL; AF004148; AAC53461.1; JOINED.
DR EMBL; AF004149; AAC53461.1; JOINED.
DR EMBL; AF004150; AAC53461.1; JOINED.
DR EMBL; AF004151; AAC53461.1; JOINED.
DR EMBL; AF004152; AAC53461.1; JOINED.
DR EMBL; AF004153; AAC53461.1; JOINED.
DR EMBL; AF004154; AAC53461.1; JOINED.
DR EMBL; AK034087; BAC28578.1; -.
DR EMBL; AK076395; BAC36320.1; -.
DR EMBL; AK033471; BAC28305.1; -.
DR EMBL; AK017853; BAB30975.1; -.
DR EMBL; BC026139; AAH26139.1; -.
DR EMBL; X95580; CAA64833.1; -.
DR EMBL; X95002; CAA64458.1; -.
DR PIR; JC4837; JC4837.
DR TRANSFAC; T04666; -.
DR MGD; MGI:106918; Hif1a.
DR GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.

Query Match 63.5%; Score 101; DB 1; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              ||||||||||||||||||||
Db        569 DLDLEMLAPYIPMDDDFQL 587


RESULT 16
Q9QX54
ID   Q9QX54      PRELIMINARY;      PRT;   630 AA.
AC   Q9QX54;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia-inducible factor 3 alpha (Fragment).
GN   Name=Hif3a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT   "Cloning and Characterization of a Third Hypoxia Inducible Factor,
RT   HIF3-alpha.";
RL   J. Biol. Chem. 0:0-0(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99054547; PubMed=9840812;
RA   Gu Y.Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT   "Molecular characterization and chromosomal localization of a third
RT   alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL   Gene Expr. 7:205-213(1998).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF079153; AAF21782.1; -.
DR   EMBL; AF079140; AAF21782.1; JOINED.
DR   EMBL; AF079141; AAF21782.1; JOINED.
DR   EMBL; AF079143; AAF21782.1; JOINED.
DR   EMBL; AF079145; AAF21782.1; JOINED.
DR   EMBL; AF079147; AAF21782.1; JOINED.
DR   EMBL; AF079149; AAF21782.1; JOINED.
DR   EMBL; AF079151; AAF21782.1; JOINED.
DR   EMBL; AF079152; AAF21782.1; JOINED.
DR   EMBL; AF079150; AAF21782.1; JOINED.
DR   EMBL; AF079148; AAF21782.1; JOINED.
DR   EMBL; AF079146; AAF21782.1; JOINED.
DR   EMBL; AF079144; AAF21782.1; JOINED.
DR   EMBL; AF079142; AAF21782.1; JOINED.
DR   HSSP; Q99814; 1P97.
DR   MGD; MGI:1859778; Hif3a.
DR   GO; GO:0005634; C:nucleus; IC.
DR   GO; GO:0003700; F:transcription factor activity; IPI.
DR   GO; GO:0001666; P:response to hypoxia; IDA.
DR   GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
FT   NON_TER     630     630
SQ   SEQUENCE   630 AA;  69623 MW;  828EB2CB4E6D45B6 CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 630;
  Best Local Similarity   94.4%;  Pred. No. 0.00098;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              ||||||||||| |||||||
Db        480 LDLEMLAPYISMDDDFQL 497


RESULT 17
Q8WXA1
ID   Q8WXA1      PRELIMINARY;      PRT;   632 AA.
AC   Q8WXA1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Inhibitory PAS domain protein.
GN   Name=IPAS;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheng J.Q.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF463492; AAL69947.1; -.
DR   HSSP; Q16665; 1LQB.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   632 AA;  68963 MW;  9665B0AF3998F8EF CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 632;
  Best Local Similarity   94.4%;  Pred. No. 0.00099;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              ||||||||||| |||||||
Db        485 LDLEMLAPYISMDDDFQL 502


RESULT 18
Q6STN6
ID   Q6STN6      PRELIMINARY;      PRT;   643 AA.
AC   Q6STN6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia-inducible factor-4alpha.
GN   Name=hif-4alpha;
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY450270; AAR95698.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
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DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   643 AA;  72434 MW;  D73C6DDD10086C4D CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 643;
  Best Local Similarity   63.0%;  Pred. No. 0.001;
  Matches   17;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 KKRRQRRRDLDLEMLAPYIPMDDDFQL 30
              | : :   :|||:|||||| |||||||
Db        487 KGQSEAMDELDLDMLAPYISMDDDFQL 513


RESULT 19
Q9HAI2
ID   Q9HAI2      PRELIMINARY;      PRT;   648 AA.
AC   Q9HAI2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ11591.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole embryo;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
DR   EMBL; AK021653; BAB13865.1; -.
DR   HSSP; Q16665; 1LQB.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00989; PAS; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   648 AA;  69995 MW;  EBEFC744BC3F148E CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 648;
  Best Local Similarity   94.4%;  Pred. No. 0.001;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| |||||||
Db        429 LDLEMLAPYISMDDDFQL 446


RESULT 20
Q9Z2I5
ID   Q9Z2I5      PRELIMINARY;      PRT;   662 AA.
AC   Q9Z2I5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia inducible factor three alpha.
GN   Name=Hif3a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99054547; PubMed=9840812;
RA   Gu Y.Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT   "Molecular characterization and chromosomal localization of a third
RT   alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL   Gene Expr. 7:205-213(1998).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF060194; AAC72734.1; -.
DR   HSSP; Q99814; 1P97.
DR   MGD; MGI:1859778; Hif3a.
DR   GO; GO:0005634; C:nucleus; IC.
DR   GO; GO:0003700; F:transcription factor activity; IPI.
DR   GO; GO:0001666; P:response to hypoxia; IDA.
DR   GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   662 AA;  73012 MW;  58740A1B6993D3B5 CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 662;
  Best Local Similarity   94.4%;  Pred. No. 0.001;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| |||||||
Db        480 LDLEMLAPYISMDDDFQL 497


RESULT 21
Q9Y2N7
ID   Q9Y2N7      PRELIMINARY;      PRT;   667 AA.
AC   Q9Y2N7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative homolog of hypoxia inducible factor three alpha (Hypoxia-
DE   inducible factor-3 alpha).
GN   Name=HIF-3A;
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA   Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA   Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA   Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA   Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA   Olsen A.S., Carrano A.V.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=21458277; PubMed=11573933; DOI=10.1006/bbrc.2001.5659;
RA   Hara S., Hamada J., Kobayashi C., Kondo Y., Imura N.;
RT   "Expression and characterization of hypoxia-inducible factor (HIF)-
RT   3alpha in human kidney: suppression of HIF-mediated gene expression by
RT   HIF-3alpha.";
RL   Biochem. Biophys. Res. Commun. 287:808-813(2001).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AC007193; AAD22668.1; -.
DR   EMBL; AB054067; BAB69689.1; -.
DR   PIR; JC7771; JC7771.
DR   HSSP; Q16665; 1LQB.
DR   Genew; HGNC:15825; HIF3A.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   667 AA;  72404 MW;  67B8794FF9DCCF4B CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 667;
  Best Local Similarity   94.4%;  Pred. No. 0.001;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| |||||||
Db        483 LDLEMLAPYISMDDDFQL 500


RESULT 22
Q66K72
ID   Q66K72      PRELIMINARY;      PRT;   669 AA.
AC   Q66K72;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   HIF3A protein.
GN   Name=HIF3A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC080551; AAH80551.1; -.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   669 AA;  72460 MW;  7EF7362A1691AE6D CRC64;

  Query Match             54.7%;  Score 87;  DB 2;  Length 669;
  Best Local Similarity   94.4%;  Pred. No. 0.0011;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| |||||||
Db        485 LDLEMLAPYISMDDDFQL 502


RESULT 23
Q7T2E4
ID   Q7T2E4      PRELIMINARY;      PRT;   571 AA.
AC   Q7T2E4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein hif1al.
GN   Name=hif1al;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054582; AAH54582.1; -.
DR   HSSP; Q99814; 1P97.
DR   ZFIN; ZDB-GENE-040426-1315; hif1al.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   571 AA;  63846 MW;  1BA8E4CC29F16672 CRC64;

  Query Match             54.1%;  Score 86;  DB 2;  Length 571;
  Best Local Similarity   84.2%;  Pred. No. 0.0012;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              :|||:|||||| |||||||
Db        430 ELDLDMLAPYISMDDDFQL 448


RESULT 24
Q6EGR9
ID   Q6EGR9      PRELIMINARY;      PRT;   626 AA.
AC   Q6EGR9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hif3a.
GN   Name=hif3a;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang C.-R., Hu C.-H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY330295; AAQ94179.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   626 AA;  70221 MW;  EA12390DFECF90B9 CRC64;

  Query Match             54.1%;  Score 86;  DB 2;  Length 626;
  Best Local Similarity   84.2%;  Pred. No. 0.0014;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAPYIPMDDDFQL 30
              :|||:|||||| |||||||
Db        485 ELDLDMLAPYISMDDDFQL 503


RESULT 25
Q9JHS2
ID   Q9JHS2      PRELIMINARY;      PRT;   662 AA.
AC   Q9JHS2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia inducible factor 3 alpha.
GN   Name=Hif-3a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA   Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;
RT   "Perivenous expression of the mRNA of the three hypoxia-inducible
RT   factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL   Biochem. J. 354:531-537(2001).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AJ277827; CAB96611.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   662 AA;  72887 MW;  AC9672E340544010 CRC64;

  Query Match             53.1%;  Score 84.5;  DB 2;  Length 662;
  Best Local Similarity   52.8%;  Pred. No. 0.0024;
  Matches   19;  Conservative    2;  Mismatches    6;  Indels    9;  Gaps    1;

Qy          4 KKRRQRRRDL---------DLEMLAPYIPMDDDFQL 30
              :| :    ||         ||||||||| |||||||
Db        462 RKNKTMETDLDIAQDPDTPDLEMLAPYISMDDDFQL 497


RESULT 26
Q6GQ12
ID   Q6GQ12      PRELIMINARY;      PRT;   859 AA.
AC   Q6GQ12;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE   MGC80468 protein.
GN   Name=MGC80468;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC072936; AAH72936.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   859 AA;  96956 MW;  59D477E1929A0AD6 CRC64;

  Query Match             51.9%;  Score 82.5;  DB 2;  Length 859;
  Best Local Similarity   81.0%;  Pred. No. 0.0062;
  Matches   17;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         11 RDLDLEMLAPYIPMD-DDFQL 30
              :||||| |||||||| :||||
Db        516 KDLDLETLAPYIPMDGEDFQL 536
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RESULT 27
Q696W2
ID   Q696W2      PRELIMINARY;      PRT;   835 AA.
AC   Q696W2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypoxia-inducible factor 2 alpha.
GN   Name=hif-2alpha;
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Law S.H.W., Kong R.Y.C., Wu R.S.S.;
RT   "Molecular characterization of hypoxia-inducible factor-2alpha (hif-
RT   2alpha) gene in grass carp.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY577524; AAT76668.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   835 AA;  92830 MW;  CAE59E9AAFC785FD CRC64;

  Query Match             50.6%;  Score 80.5;  DB 2;  Length 835;
  Best Local Similarity   85.0%;  Pred. No. 0.012;
  Matches   17;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              ||||| |||||||| :||||
Db        518 DLDLETLAPYIPMDGEDFQL 537
```

```
RESULT 28
Q6GL61
ID   Q6GL61      PRELIMINARY;      PRT;   862 AA.
AC   Q6GL61;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Epas1-prov protein.
GN   Name=epas1-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC074648; AAH74648.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   862 AA;  97138 MW;  C2976D62101531CE CRC64;

  Query Match             50.6%;  Score 80.5;  DB 2;  Length 862;
  Best Local Similarity   85.0%;  Pred. No. 0.012;
  Matches   17;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              ||||| |||||||| :||||
Db        517 DLDLETLAPYIPMDGEDFQL 536


RESULT 29
Q6GP97
ID   Q6GP97      PRELIMINARY;      PRT;   862 AA.
AC   Q6GP97;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80589 protein.
GN   Name=MGC80589;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC073244; AAH73244.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   862 AA;  97319 MW;  3AC8FB39032E9E60 CRC64;

  Query Match             50.6%;  Score 80.5;  DB 2;  Length 862;
  Best Local Similarity   85.0%;  Pred. No. 0.012;
  Matches   17;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              ||||| |||||||| :||||
Db        518 DLDLETLAPYIPMDGEDFQL 537


RESULT 30
Q8QGM4
ID   Q8QGM4      PRELIMINARY;      PRT;   873 AA.
AC   Q8QGM4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia-inducible factor 2 alpha.
OS   Fundulus heteroclitus (Killifish) (Mummichog).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Cyprinodontiformes; Fundulidae; Fundulus.
OX   NCBI_TaxID=8078;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
RA   Powell W.H., Hahn M.E.;
RT   "Identification and functional characterization of Hypoxia-inducible
RT   factor 2alpha from the estuaring teleost, Fundulus heteroclitus:
RT   Interaction of HIF2a with two ARNT2 splice variants.";
RL   J. Exp. Zool. 294:17-29(2002).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF402782; AAL95711.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   873 AA;  96437 MW;  BA2CF40AB4ABC7B0 CRC64;

  Query Match           50.6%;  Score 80.5;  DB 2;  Length 873;
  Best Local Similarity   85.0%;  Pred. No. 0.012;
  Matches   17;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              ||||| |||||||| :||||
Db        541 DLDLETLAPYIPMDGEDFQL 560


RESULT 31
Q96K34
ID   Q96K34      PRELIMINARY;      PRT;   632 AA.
AC   Q96K34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ14819.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AK027725; BAB55324.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   632 AA;  68933 MW;  A19F1ED3D05E7A71 CRC64;

  Query Match           50.3%;  Score 80;  DB 2;  Length 632;
  Best Local Similarity   88.9%;  Pred. No. 0.01;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAPYIPMDDDFQL 30
              |||||||||| | |||||
Db        485 LDLEMLAPYISMGDDFQL 502


RESULT 32
Q6RYD1
ID   Q6RYD1      PRELIMINARY;      PRT;   163 AA.
AC   Q6RYD1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Endothelial PAS domain protein 1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ing N.H., Balog C.J., Wolfskill R.L.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY485673; AAR37390.1; -.
FT   NON_TER       1      1
FT   NON_TER     163    163
SQ   SEQUENCE   163 AA;  17207 MW;  679CDA9F183CCAD3 CRC64;

  Query Match           48.1%;  Score 76.5;  DB 2;  Length 163;
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  Best Local Similarity   80.0%;  Pred. No. 0.0068;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        118 ELDLETLAPYIPMDGEDFQL 137


RESULT 33
Q6RYD0
ID   Q6RYD0      PRELIMINARY;      PRT;   164 AA.
AC   Q6RYD0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Endothelial PAS domain protein 1 (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ing N.H., Balog C.J., Wolfskill R.L.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY485674; AAR37391.1; -.
FT   NON_TER       1      1
FT   NON_TER     164    164
SQ   SEQUENCE   164 AA;  17405 MW;  49DBB95BA3D6D826 CRC64;

  Query Match             48.1%;  Score 76.5;  DB 2;  Length 164;
  Best Local Similarity   80.0%;  Pred. No. 0.0069;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        119 ELDLETLAPYIPMDGEDFQL 138


RESULT 34
Q9W7C6
ID   Q9W7C6      PRELIMINARY;      PRT;   867 AA.
AC   Q9W7C6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Endothelial PAS domain protein 1.
GN   Name=EPAS1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=breed White Leghorn;
RX   MEDLINE=20047819; PubMed=10580084; DOI=10.1016/S0014-5793(99)01476-3;
RA   Favier J., Kempf H., Corvol P., Gasc J.-M.;
RT   "Cloning and expression pattern of EPAS1 in the chicken embryo.
RT   Colocalization with tyrosine hydroxylase.";
RL   FEBS Lett. 462:19-24(1999).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF129813; AAD38358.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   867 AA;  97133 MW;  DE674A948DE11DCC CRC64;

  Query Match             48.1%;  Score 76.5;  DB 2;  Length 867;
  Best Local Similarity   80.0%;  Pred. No. 0.045;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 35
PAS1_HUMAN
ID   PAS1_HUMAN      STANDARD;      PRT;   870 AA.
AC   Q99814; Q86VA2; Q99630;
DT   15-DEC-1998 (Rel. 37, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2)
DE   (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha)
DE   (HIF-1 alpha-like factor) (HLF).
GN   Name=EPAS1; Synonyms=HIF2A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97152468; PubMed=9000051;
RA   Tian H., McKnight S.L., Russell D.W.;
RT   "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT   selectively expressed in endothelial cells.";
RL   Genes Dev. 11:72-82(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hepatoma;
RX   MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA   Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA   Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT   "Characterization of a subset of the basic-helix-loop-helix-PAS
RT   superfamily that interacts with components of the dioxin signaling
RT   pathway.";
RL   J. Biol. Chem. 272:8581-8593(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP   MUTAGENESIS OF CYS-844.
RX   MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA   Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA   Poellinger L., Fujii-Kuriyama Y.;
RT   "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT   in response to hypoxia: their stabilization and redox signal-induced
RT   interaction with CBP/p300.";
RL   EMBO J. 18:1905-1914(1999).
CC   -!- FUNCTION: Transcription factor involved in the induction of oxygen
CC       regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
CC       the hypoxia response element (HRE) of target gene promoters.
CC       Regulates the vascular endothelial growth factor (VEGF) expression
CC       and seems to be implicated in the development of blood vessels and
CC       the tubular system of lung. May also play a role in the formation
CC       of the endothelium that gives rise to the blood brain barrier.
CC       Potent activator of the Tie-2 tyrosine kinase expression.
CC       Activation seems to require recruitment of transcriptional
CC       coactivators such as CREBPB and probably EP300. Interaction with
CC       redox regulatory protein APEX seems to activate CTAD.
CC   -!- SUBUNIT: Efficient DNA binding requires dimerization wih another
CC       bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
CC       in placenta, lung and heart. Selectively expressed in endothelial
CC       cells.
CC   -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-531
CC       by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
CC       prolines promote interaction with VHL, initiating rapid
CC       ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-847 by HIF1AN thus
CC       probably abrogating interaction with CREBBP and EP300 and
CC       preventing transcriptional activation (By similarity).
CC   -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U81984; AAB41495.1; -.
DR   EMBL; U51626; AAC51212.1; -.
DR   EMBL; BC051338; AAH51338.1; -.
DR   PDB; 1P97; NMR; A=237-350.
DR   TRANSFAC; T02718; -.
DR   Genew; HGNC:3374; EPAS1.
DR   MIM; 603349; -.
DR   GO; GO:0003705; F:RNA polymerase II transcription factor acti. . .; TAS.
DR   GO; GO:0003713; F:transcription coactivator activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0006366; P:transcription from Pol II promoter; TAS.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   3D-structure; Activator; Angiogenesis; Developmental protein;
KW   DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW   Transcription regulation.
FT   DNA_BIND      15     27       Basic motif.
FT   DOMAIN        28     68       Helix-loop-helix motif.
FT   DOMAIN        84    154       PAS 1.
FT   DOMAIN       230    300       PAS 2.
FT   DOMAIN       304    347       PAC.
FT   DOMAIN       496    542       NTAD.
FT   DOMAIN       830    870       CTAD.
FT   DOMAIN       474    480       Poly-Ser.
FT   MOD_RES      405    405       Hydroxyproline (By similarity).
FT   MOD_RES      531    531       Hydroxyproline (By similarity).
FT   MOD_RES      840    840       Phosphothreonine (By similarity).
FT   MOD_RES      847    847       3-hydroxyasparagine (By similarity).
FT   MUTAGEN      844    844       C->S: Abolishes hypoxia-inducible
FT                                 transcriptional activation of ctaD.
FT   CONFLICT      60     60       A -> E (in Ref. 1).
FT   CONFLICT     539    539       D -> G (in Ref. 2).
FT   CONFLICT     601    601       H -> R (in Ref. 2).
FT   CONFLICT     693    693       D -> N (in Ref. 2).
FT   CONFLICT     716    716       E -> K (in Ref. 2).
FT   CONFLICT     722    722       L -> P (in Ref. 2).
FT   CONFLICT     765    765       F -> L (in Ref. 2).
FT   CONFLICT     769    769       P -> S (in Ref. 2).
FT   CONFLICT     844    844       C -> R (in Ref. 2).
FT   CONFLICT     847    847       N -> K (in Ref. 2).
SQ   SEQUENCE   870 AA;  96458 MW;  4838989598234FC1 CRC64;

  Query Match             48.1%;  Score 76.5;  DB 1;  Length 870;
  Best Local Similarity   80.0%;  Pred. No. 0.046;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 36
Q9XTA4
ID   Q9XTA4      PRELIMINARY;      PRT;   870 AA.
AC   Q9XTA4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Endothelial PAS domain protein 1/hypoxia-inducible factor-2
DE   alpha.
GN   Name=EPAS1/HIF2 alpha;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Arterial;
RX   MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA   Hara S., Kobayashi C., Imura N.;
RT   "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-
RT   1alpha and -2alpha of bovine arterial endothelial cells.";
RL   Biochim. Biophys. Acta 1445:237-243(1999).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AB018399; BAA78676.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
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DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   870 AA;  96168 MW;  FEC602E6012D7712 CRC64;

  Query Match             48.1%;  Score 76.5;  DB 2;  Length 870;
  Best Local Similarity   80.0%;  Pred. No. 0.046;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 37
Q9PTB3
ID   Q9PTB3      PRELIMINARY;      PRT;   870 AA.
AC   Q9PTB3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia-inducible factor 2 alpha.
OS   Coturnix coturnix (Common quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=9091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99425185; PubMed=10495286; DOI=10.1016/S0925-4773(99)00144-6;
RA   Elvert G., Lanz S., Kappel A., Flamme I.;
RT   "mRNA cloning and expression studies of the quail homolog of HIF-2
RT   alpha.";
RL   Mech. Dev. 87:193-197(1999).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF212989; AAF21052.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   870 AA;  97803 MW;  086AC8CF1639D77C CRC64;

  Query Match             48.1%;  Score 76.5;  DB 2;  Length 870;
  Best Local Similarity   80.0%;  Pred. No. 0.046;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 38
PAS1_MOUSE
ID   PAS1_MOUSE     STANDARD;      PRT;   874 AA.
AC   P97481; O08787; O55046;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2
DE   alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (MHLF)
DE   (HIF-related factor) (HRF).
GN   Name=Epas1; Synonyms=Hif2a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97152468; PubMed=9000051;
RA   Tian H., McKnight S.L., Russell D.W.;
RT   "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT   selectively expressed in endothelial cells.";
RL   Genes Dev. 11:72-82(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Hypothalamus, and Skeletal muscle;
RX   MEDLINE=97272213; PubMed=9113979; DOI=10.1073/pnas.94.9.4273;
RA   Ema M., Taya S., Yokotani N., Sogawa K., Matsuda Y.,
RA   Fujii-Kuriyama Y.;
RT   "A novel bHLH-PAS factor with close sequence similarity to hypoxia-
RT   inducible factor 1alpha regulates the VEGF expression and is
RT   potentially involved in lung and vascular development.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain capillary;
RX   MEDLINE=97321546; PubMed=9178256; DOI=10.1016/S0925-4773(97)00674-6;
RA   Flamme I., Froehlich T., von Reutern M., Kappel A., Damert A.,
RA   Risau W.;
RT   "HRF, a putative basic helix-loop-helix-PAS-domain transcription
RT   factor is closely related to hypoxia-inducible factor-1 alpha and
RT   developmentally expressed in blood vessels.";
RL   Mech. Dev. 63:51-60(1997).
RN   [4]
RP   SEQUENCE OF 846-864, AND MUTAGENESIS OF PRO-530 AND ASN-851.
RX   MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA   Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA   Bruick R.K.;
RT   "FIH-1 is an asparaginyl hydroxylase enzyme that regulates the
RT   transcriptional activity of hypoxia-inducible factor.";
RL   Genes Dev. 16:1466-1471(2002).
RN   [5]
RP   INTERACTION WITH CREBBP, PHOSPHORYLATION SITE THR-844, AND MUTAGENESIS
RP   OF THR-844.
RX   MEDLINE=22075202; PubMed=11983697; DOI=10.1074/jbc.M201307200;
RA   Gradin K., Takasaki C., Fujii-Kuriyama Y., Sogawa K.;
RT   "The transcriptional activation function of the HIF-like factor
RT   requires phosphorylation at a conserved threonine.";
RL   J. Biol. Chem. 277:23508-23514(2002).
RN   [6]
RP   HYDROXYLATION OF ASN-851.
RX   MEDLINE=21682001; PubMed=11823643; DOI=10.1126/science.1068592;
RA   Lando D., Peet D.J., Whelan D.A., Gorman J.J., Whitelaw M.L.;
RT   "Asparagine hydroxylation of the HIF transactivation domain a hypoxic
RT   switch.";
RL   Science 295:858-861(2002).
CC   -!- FUNCTION: Transcription factor involved in the induction of oxygen
CC       regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
CC       the hypoxia response element (HRE) of target gene promoters.
CC       Regulates the vascular endothelial growth factor (VEGF) expression
CC       and seems to be implicated in the development of blood vessels and
```

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CC       the tubular system of lung. May also play a role in the formation
CC       of the endothelium that gives rise to the blood brain barrier.
CC       Potent activator of the Tie-2 tyrosine kinase expression.
CC       Activation requires recruitment of transcriptional coactivators
CC       such as CREBPB and probably EP300. Interaction with redox
CC       regulatory protein APEX seems to activate CTAD (By similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires dimerization wih another
CC       bHLH protein. Heterodimerizes with ARNT. Interacts with CREBPB.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
CC       in lung, followed by heart, kidney, brain and liver. Predominantly
CC       expressed in endothelial cells. Also found in smooth muscle cells
CC       of the uterus, neurons, and brown adipose tissue. High expression
CC       in embryonic choroid plexus and kidney glomeruli.
CC   -!- DEVELOPMENTAL STAGE: In day 11 embryo, expression is almost
CC       exclusively seen in endothelial cells of the intersegmental blood
CC       vessels separating the somites, the atrial and ventricular
CC       chambers of the heart, and the dorsal aorta. High expression also
CC       occurs in extra-embryonic membranes. In the developing brain of
CC       day 13 embryo, endothelial cells of the highly vascularized
CC       choroid plexus contain high levels of EPAS1.
CC   -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530
CC       by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
CC       prolines promote interaction with VHL, initiating rapid
CC       ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus
CC       probably abrogating interaction with CREBBP and EP300 and
CC       preventing transcriptional activation.
CC   -!- PTM: Phosphorylated on multiple sites in the CTAD.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U81983; AAB41496.1; -.
DR   EMBL; D89787; BAA20130.1; -.
DR   EMBL; AF045160; AAC12871.1; -.
DR   HSSP; Q16665; 1H2K.
DR   TRANSFAC; T02719; -.
DR   MGD; MGI:109169; Epas1.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   TIGRFAMs; TIGR00229; sensory_box; 2.
DR   PROSITE; PS50888; HLH; FALSE_NEG.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; Angiogenesis; Developmental protein;
KW   Direct protein sequencing; DNA-binding; Hydroxylation;
KW   Nuclear protein; Phosphorylation; Repeat; Transcription regulation.
FT   DNA_BIND      15     27       Basic motif.
FT   DOMAIN        28     68       Helix-loop-helix motif.
FT   DOMAIN        84    154       PAS 1.
FT   DOMAIN       230    300       PAS 2.
FT   DOMAIN       304    347       PAC.
FT   DOMAIN       495    541       NTAD.
FT   DOMAIN       834    874       CTAD.
FT   DOMAIN       471    479       Poly-Ser.
FT   MOD_RES      405    405       Hydroxyproline (By similarity).
FT   MOD_RES      530    530       Hydroxyproline (By similarity).
FT   MOD_RES      844    844       Phosphothreonine.
FT   MOD_RES      851    851       3-hydroxyasparagine.
FT   MUTAGEN      530    530       P->A: Confers transcriptional activity at
FT                                 normoxia; when associated with A-851.
FT   MUTAGEN      844    844       T->A: Decreases interaction with CREBBP.
FT   MUTAGEN      851    851       N->A: Confers transcriptional activity at
FT                                 normoxia; when associated with A-530.
FT   CONFLICT      25     25       C -> S (in Ref. 2).
FT   CONFLICT     191    191       K -> KS (in Ref. 1).
FT   CONFLICT     439    440       VS -> AA (in Ref. 3).
FT   CONFLICT     463    463       D -> G (in Ref. 3).
FT   CONFLICT     654    654       G -> V (in Ref. 2).
FT   CONFLICT     663    663       A -> P (in Ref. 2).
FT   CONFLICT     669    669       S -> W (in Ref. 1).
FT   CONFLICT     673    673       P -> L (in Ref. 1).
FT   CONFLICT     678    678       P -> L (in Ref. 1).
FT   CONFLICT     725    725       D -> E (in Ref. 3).
FT   CONFLICT     731    731       P -> L (in Ref. 3).
FT   CONFLICT     762    762       A -> G (in Ref. 3).
FT   CONFLICT     786    786       P -> L (in Ref. 3).
FT   CONFLICT     791    791       S -> F (in Ref. 3).
FT   CONFLICT     794    794       S -> N (in Ref. 3).
SQ   SEQUENCE   874 AA;  96712 MW;  A6FFA490AE43640C CRC64;

  Query Match             48.1%;  Score 76.5;  DB 1;  Length 874;
  Best Local Similarity   80.0%;  Pred. No. 0.046;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 39
PAS1_RAT
ID   PAS1_RAT       STANDARD;      PRT;   874 AA.
AC   Q9JHS1;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2
DE   alpha) (HIF-2 alpha) (HIF2 alpha).
GN   Name=Epas1; Synonyms=Hif2a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA   Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;
RT   "Perivenous expression of the mRNA of the three hypoxia-inducible
RT   factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL   Biochem. J. 354:531-537(2001).
CC   -!- FUNCTION: Transcription factor involved in the induction of oxygen
CC       regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
CC       the hypoxia response element (HRE) of target gene promoters.
CC       Regulates the vascular endothelial growth factor (VEGF) expression
CC       and seems to be implicated in the development of blood vessels and
CC       the tubular system of lung. May also play a role in the formation
CC       of the endothelium that gives rise to the blood brain barrier.
CC       Potent activator of the Tie-2 tyrosine kinase expression.
CC       Activation seems to require recruitment of transcriptional
CC       coactivators such as CREBPB and probably EP300. Interaction with
CC       redox regulatory protein APEX seems to activate CTAD (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires dimerization wih another
CC       bHLH protein. Heterodimerizes with ARNT (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
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CC   -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530
CC       by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
CC       prolines promote interaction with VHL, initiating rapid
CC       ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus
CC       probably abrogating interaction with CREBBP and EP300 and
CC       preventing transcriptional activation (By similarity).
CC   -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277828; CAB96612.1; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   TIGRFAMs; TIGR00229; sensory_box; 2.
DR   PROSITE; PS50888; HLH; FALSE_NEG.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; Angiogenesis; Developmental protein; DNA-binding;
KW   Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW   Transcription regulation.
FT   DNA_BIND      15     27       Basic motif.
FT   DOMAIN        28     68       Helix-loop-helix motif.
FT   DOMAIN        84    154       PAS 1.
FT   DOMAIN       230    300       PAS 2.
FT   DOMAIN       304    347       PAC.
FT   DOMAIN       495    541       NTAD.
FT   DOMAIN       834    874       CTAD.
FT   DOMAIN       474    479       Poly-Ser.
FT   MOD_RES      405    405       Hydroxyproline (By similarity).
FT   MOD_RES      530    530       Hydroxyproline (By similarity).
FT   MOD_RES      844    844       Phosphothreonine (By similarity).
FT   MOD_RES      851    851       3-hydroxyasparagine (By similarity).
SQ   SEQUENCE   874 AA;  96718 MW;  A1FF08EB24369796 CRC64;

  Query Match             48.1%;  Score 76.5;  DB 1;  Length 874;
  Best Local Similarity   80.0%;  Pred. No. 0.046;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 40
Q6PEU2
ID   Q6PEU2      PRELIMINARY;      PRT;   874 AA.
AC   Q6PEU2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Endothelial PAS domain protein 1.
GN   Name=Epas1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC057870; AAH57870.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   874 AA;  96636 MW;  2E6D7603A678EACE CRC64;

  Query Match             48.1%;  Score 76.5;  DB 2;  Length 874;
  Best Local Similarity   80.0%;  Pred. No. 0.046;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAPYIPMD-DDFQL 30
              :|||| |||||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 41
Q8QGI5
ID   Q8QGI5      PRELIMINARY;      PRT;   235 AA.
AC   Q8QGI5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypoxia-inducible factor alpha-like protein (Fragment).
OS   Fundulus heteroclitus (Killifish) (Mummichog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Cyprinodontiformes; Fundulidae; Fundulus.
OX   NCBI_TaxID=8078;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
RA   Powell W.H., Hahn M.E.;
RT   "Identification and functional characterization of hypoxia-inducible
RT   factor 2alpha from the estuarine teleost, Fundulus heteroclitus:
RT   interaction of HIF-2alpha with two ARNT2 splice variants.";
RL   J. Exp. Zool. 294:17-29(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Oleksiak M.F., Kolell K.J., Crawford D.L., Hahn M.E., Powell W.H.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF433668; AAM12473.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001610; PAC.
DR   SMART; SM00086; PAC; 1.
FT   NON_TER       1      1
FT   NON_TER     235    235
SQ   SEQUENCE   235 AA;  25400 MW;  AE7A7C5D15827351 CRC64;

  Query Match           40.9%;  Score 65;  DB 2;  Length 235;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 DLEMLAPYIPMDDDF 28
              :||| |||| |||||
Db        221 ELEMYAPYISMDDDF 235


RESULT 42
Q6GXZ1
ID   Q6GXZ1      PRELIMINARY;      PRT;    72 AA.
AC   Q6GXZ1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Tat protein (Fragment).
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Eric L., Kumar R., Hill M.D., Costas S., Chaudhary S., Tirado G.,
RA   Yamamura Y., Kumar A.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AY620859; AAT48062.1; -.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      72     72
SQ   SEQUENCE   72 AA;  8397 MW;  9D83E7DB3486EC2B CRC64;

  Query Match           40.6%;  Score 64.5;  DB 2;  Length 72;
  Best Local Similarity   53.3%;  Pred. No. 0.14;
  Matches   16;  Conservative    0;  Mismatches    7;  Indels    7;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30
              ||||||||||        ||    ||   |
Db         47 YGRKKRRQRRR-------APRDSQDDQVSL 69


RESULT 43
Q71939
ID   Q71939      PRELIMINARY;      PRT;    71 AA.
AC   Q71939;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Michael N.L.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U24453; AAA79589.1; -.
DR   HSSP; P12506; 1TBC.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      71     71
SQ   SEQUENCE   71 AA;  8307 MW;  A3EFC2840AFF2A50 CRC64;

  Query Match           39.3%;  Score 62.5;  DB 2;  Length 71;
  Best Local Similarity   58.3%;  Pred. No. 0.27;
  Matches   14;  Conservative    2;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAPYIP 23
              ||||||||||   | :    |:|
Db         47 YGRKKRRQRRRAPQDSQTYQAYLP 70


RESULT 44
Q71945
ID   Q71945      PRELIMINARY;      PRT;    71 AA.
AC   Q71945;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Michael N.L.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
```

```
DR   EMBL; U24454; AAA79595.1; -.
DR   HSSP; P12506; 1TBC.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      71     71
SQ   SEQUENCE   71 AA;  8307 MW;  A3EFC2840AFF2A50 CRC64;

  Query Match             39.3%;  Score 62.5;  DB 2;  Length 71;
  Best Local Similarity   58.3%;  Pred. No. 0.27;
  Matches   14;  Conservative    2;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAPYIP 23
              ||||||||||| | :  |:|
Db         47 YGRKKRRQRRRAPQDSQTYQAYLP 70


RESULT 45
Q8UT76
ID   Q8UT76      PRELIMINARY;      PRT;    99 AA.
AC   Q8UT76;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21988475; PubMed=11991972;
RX   DOI=10.1128/JVI.76.11.5435-5451.2002;
RA   Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA   Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA   Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
RA   Marlink R., Lee T.-H., Essex M.;
RT   "Human immunodeficiency virus type 1 subtype C molecular phylogeny:
RT   consensus sequence for an AIDS vaccine design?";
RL   J. Virol. 76:5435-5451(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Novitsky V.A., McLane M.F., Chigwedere P., Ndung'u T., Klein I.,
RA   Chang S.-Y., Peter T., Thior I., Rybak N., Gaseitsiwe S., Vannberg F.,
RA   Marlink R., Lee T.-H., Essex M.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AF443098; AAL34773.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   99 AA;  11224 MW;  C5AAF4550C540404 CRC64;

  Query Match             39.3%;  Score 62.5;  DB 2;  Length 99;
  Best Local Similarity   55.2%;  Pred. No. 0.4;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    9;  Gaps    2;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQ 29
              ||||||||||| |  |  :| |
Db         47 YGRKKRRQRRR-------AP--PSSEDHQ 66


RESULT 46
Q90CH6
ID   Q90CH6      PRELIMINARY;      PRT;   101 AA.
AC   Q90CH6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21342588; PubMed=11448170; DOI=10.1006/viro.2001.0976;
RA   Carr J.K., Torimiro J.N., Wolfe N.D., Eitel M.N., Kim B.,
RA   Sanders-Buell E., Jagodzinski L.L., Gotte D., Burke D.S., Birx D.L.,
RA   McCutchan F.E.;
RT   "The AG recombinant IbNG and novel strains of group M HIV-1 are common
RT   in Cameroon.";
RL   Virology 286:168-181(2001).
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AF377958; AAK59208.1; -.
DR   HSSP; P04613; 1K5K.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   101 AA;  11341 MW;  DB0905BA91551BD8 CRC64;

  Query Match             39.3%;  Score 62.5;  DB 2;  Length 101;
  Best Local Similarity   55.2%;  Pred. No. 0.41;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    9;  Gaps    2;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQ 29
              ||||||||||| |  |  :| |
Db         47 YGRKKRRQRRR-------AP--PSSEDHQ 66


RESULT 47
Q90CY2
ID   Q90CY2      PRELIMINARY;      PRT;   101 AA.
AC   Q90CY2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21395692; PubMed=11504977;
RA   Hoelscher M., Kim B., Maboko L., Mhalu F., von Sonnenburg F.,
RA   Birx D.L., McCutchan F.E.,
RA   the UNAIDS Network for HIV Isolation Characterization.;
RT   "High proportion of unrelated HIV-1 intersubtype recombinants in the
RT   Mbeya region of southwest Tanzania.";
RL   AIDS 15:1461-1470(2001).
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
```

```
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AF361876; AAK94259.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   101 AA;  11534 MW;  54592B65F004E284 CRC64;

  Query Match           39.3%;  Score 62.5;  DB 2;  Length 101;
  Best Local Similarity   55.2%;  Pred. No. 0.41;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    9;  Gaps    2;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQ 29
              ||||||||||        ||  |  :| |
Db         47 YGRKKRRQRRR-------AP--PSSEDHQ 66


RESULT 48
Q8ADC2
ID   Q8ADC2      PRELIMINARY;      PRT;    86 AA.
AC   Q8ADC2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325;
RA   Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA   Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
RA   Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA   McCutchan F.E.;
RT   "Among 46 near full length HIV type 1 genome sequences from Rakai
RT   District, Uganda, subtype D and AD recombinants predominate.";
RL   AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harris M.E., Birx D.L., Robb M.L.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Lutalo T.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Meehen M., Wawer M.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AF484516; AAN73784.1; -.
DR   HSSP; P04613; 1K5K.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   86 AA;  9905 MW;  01C995B36AE0161A CRC64;

  Query Match           39.0%;  Score 62;  DB 2;  Length 86;
  Best Local Similarity   53.8%;  Pred. No. 0.4;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels   10;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDD 26
              ||||||||||          | ||
Db         47 YGRKKRRQRRRS----------PQDD 62


RESULT 49
Q69628
ID   Q69628      PRELIMINARY;      PRT;    72 AA.
AC   Q69628;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95264414; PubMed=7745674;
RA   Diaz R.S., Sabino E.C., Mayer A., Mosley J.W., Busch M.P.;
RT   "Dual human immunodeficiency virus type 1 infection and recombination
RT   in a dually exposed transfusion recipient. The Transfusion Safety
RT   Study Group.";
RL   J. Virol. 69:3273-3281(1995).
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U11191; AAA78877.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      72      72
SQ   SEQUENCE   72 AA;  8428 MW;  4A00C4BF893D0E86 CRC64;

  Query Match           38.7%;  Score 61.5;  DB 2;  Length 72;
  Best Local Similarity   65.2%;  Pred. No. 0.39;
  Matches   15;  Conservative    1;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRDL-DLEMLAPYI 22
              ||||||||||| | | |    |:
Db         47 YGRKKRRQRRRALKDSETHQAYL 69


RESULT 50
P88699
ID   P88699      PRELIMINARY;      PRT;    72 AA.
AC   P88699;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
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DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Quinones-Mateu M.E., Domingo E.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U80465; AAB39115.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      72      72
SQ   SEQUENCE   72 AA;  8342 MW;  ED2C18A34DA4B591 CRC64;

  Query Match             38.4%;  Score 61;  DB 2;  Length 72;
  Best Local Similarity   91.7%;  Pred. No. 0.46;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRD 12
              |||||| |||||
Db         47 YGRKKRKQRRRD 58


Search completed: February  9, 2005, 06:00:14
Job time : 81.4737 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 9, 2005, 05:55:37 ; Search time 17.3684 Seconds
(without alignments)
166.193 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 159
Sequence: 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	101	63.5	810	2	JC4837	hypoxia-inducible
2	101	63.5	811	2	JC7619	hypoxia-inducible
3	101	63.5	813	2	JC5809	hypoxia-inducible
4	101	63.5	826	2	I38972	hypoxia-inducible
5	87	54.7	667	2	JC7771	hypoxia inducible
6	59	37.1	685	2	F75370	oligopeptidase A -
7	58	36.5	71	2	T09384	trans-activating t
8	58	36.5	72	1	TNLJH4	trans-activating t
9	58	36.5	86	1	TNLJZR	trans-activating t
10	58	36.5	86	2	JC5591	transactivator pro
11	58	36.5	86	2	A25700	trans-activating t
12	58	36.5	86	2	S54381	tat protein - huma
13	58	36.5	86	2	S33982	trans-activating t
14	58	36.5	87	2	T01665	tat protein - huma
15	58	36.5	95	1	TNLJ12	trans-activating t
16	58	36.5	101	1	E44001	trans-activating t
17	58	36.5	101	2	T09446	tat protein - huma
18	55	34.6	86	1	TNLJND	trans-activating t
19	54	34.0	713	2	S76766	hypothetical prote
20	54	34.0	1505	2	JC4851	hypoxia-inducible
21	51	32.1	220	1	B5AG58	virB5 protein prec
22	51	32.1	220	2	AI3248	component of type
23	50	31.4	259	1	CTXLPA	corticotropin / li
24	50	31.4	260	1	CTXLPB	corticotropin / li
25	50	31.4	276	2	B38965	hypothetical prote
26	50	31.4	457	2	D83741	hypothetical prote
27	50	31.4	561	2	E70610	hypothetical prote
28	49.5	31.1	307	2	T01773	syntaxin homolog A
29	49	30.8	422	2	F64651	hypothetical prote
30	49	30.8	440	2	G71939	hypothetical prote
31	48.5	30.5	900	2	B70694	probable infB - My
32	48.5	30.5	924	2	F87103	initiation factor
33	48	30.2	107	2	A70966	hypothetical prote
34	48	30.2	232	2	D71218	hypothetical prote
35	48	30.2	233	2	D75185	hypothetical prote
36	48	30.2	561	2	S35637	high mobility grou
37	48	30.2	840	2	S41218	HIR1 protein - yea
38	48	30.2	1021	2	A28199	Na+/K+-exchanging
39	48	30.2	1023	1	A24639	Na+/K+-exchanging
40	48	30.2	1023	2	A24414	Na+/K+-exchanging
41	48	30.2	1473	2	T13855	suppressor of sabl
42	47.5	29.9	407	2	T37242	transforming growt
43	47.5	29.9	462	2	C85651	hypothetical prote
44	47.5	29.9	462	2	H90790	hypothetical prote
45	47.5	29.9	563	2	T20192	hypothetical prote
46	47.5	29.9	878	2	S74207	lipoxygenase (EC 1
47	47	29.6	88	2	G64139	DNA-directed RNA p
48	47	29.6	124	2	B82444	hypothetical prote
49	47	29.6	279	2	A81971	lacto-N-neotetraos
50	47	29.6	344	2	I49585	CD2 antigen protei
51	47	29.6	344	2	B28967	T-cell surface gly
52	47	29.6	351	1	RWHUC2	T-cell surface gly
53	47	29.6	448	2	T03776	tat binding protei
54	47	29.6	540	2	A86020	hypothetical prote
55	47	29.6	540	2	A98174	hypothetical prote
56	47	29.6	540	2	S47708	hypothetical 61.2K
57	47	29.6	677	2	D87708	peptidyl-dipeptida
58	47	29.6	1021	1	S04630	Na+/K+-exchanging
59	47	29.6	1272	2	S26180	neurofascin - chic
60	47	29.6	1290	2	A56493	leucocyte common a
61	47	29.6	1298	2	I54367	X-linked nuclear p
62	47	29.6	1898	2	S46216	leukocyte antigen-
63	46.5	29.2	50	2	G84198	hypothetical prote
64	46.5	29.2	180	2	B97242	hypothetical prote
65	46.5	29.2	255	2	T46350	hypothetical prote

ALIGNMENTS

RESULT 1
JC4837
hypoxia-inducible factor 1 alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: JC4837
R;Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M.
Biochem. Biophys. Res. Commun. 223, 54-59, 1996
A;Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxi
A;Reference number: JC4837; MUID:96254028; PMID:8660378
A;Accession: JC4837
A;Molecule type: mRNA
A;Residues: 1-810 <WEN>
A;Cross-references: UNIPROT:Q61221; EMBL:X95580; NID:g1430864; PIDN:CAA64833.1; PID:g43
C;Comment: This factor is involved in the oxygen-regulated transcription of several gen
C;Genetics:
A;Gene: Hif1alpha
A;Map position: 12
C;Keywords: transcription factor
F;5-58/Region: helix-loop-helix #status predicted

Query Match 63.5%; Score 101; DB 2; Length 810;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 543 DLDLEMLAPYIPMDDDFQL 561

RESULT 2
JC7619

hypoxia-inducible factor 1 alpha - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7619
R;Takahashi, T.; Sugishita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kinugawa, K.; Harada,
Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001
A;Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventricul
A;Reference number: JC7619; MUID:21134360; PMID:11237772
A;Contents: Embryonic ventricular myocytes
A;Accession: JC7619
A;Molecule type: mRNA
A;Residues: 1-811 <TAK>
A;Cross-references: DDBJ:AB013746
C;Comment: This factor belongs to the basic helix-loop-helix-Per/ARNT/Sim (HLH-PAS) fami
eostasis of cells, and in redox stimuli.
C;Genetics:
A;Gene: hif-1alpha
C;Keywords: embryo; transcription factor
F;106-156/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS1>
F;249-299/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS2>
F;762-811/Domain: conserved carboxy-terminal transactivation element #status predicted <
F;767-768/Region: conserved dileucine repeat, important for oxygen-dependent degradation

Query Match 63.5%; Score 101; DB 2; Length 811;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 554 DLDLEMLAPYIPMDDDFQL 572

RESULT 3
JC5809
hypoxia-inducible factor 1 alpha - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999
C;Accession: JC5809
R;Ladoux, A.; Frelin, C.
Biochem. Biophys. Res. Commun. 240, 552-556, 1997
A;Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop helix/PAS domai
A;Reference number: JC5809; MUID:98063274; PMID:9398602
A;Accession: JC5809
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-813 <LAD>
C;Comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator
as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, e
F;6-144/Region: basic helix-loop-helix #status predicted

Query Match 63.5%; Score 101; DB 2; Length 813;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 543 DLDLEMLAPYIPMDDDFQL 561

RESULT 4
I38972
hypoxia-inducible factor 1 alpha - human
N;Alternate names: ARNT interacting protein
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38972; G01875
R;Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995
A;Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulate
A;Reference number: I38972; MUID:95296340; PMID:7539918
A;Accession: I38972
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-826 <RES>
A;Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g8813
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.
submitted to the EMBL Data Library, June 1995
A;Reference number: H00692
A;Accession: G01875
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-826 <HOG>
A;Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1; PID:g1144013
C;Genetics:
A;Gene: GDB:HIF1A
A;Cross-references: GDB:512229
A;Map position: 14q21-14q24
C;Keywords: heterodimer

Query Match 63.5%; Score 101; DB 2; Length 826;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAPYIPMDDDFQL 30
||||||||||||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 5
JC7771
hypoxia inducible factor-3 alpha - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: JC7771
R;Hara, S.; Hamada, J.; Kobayashi, C.; Kondo, Y.; Imura, N.
Biochem. Biophys. Res. Commun. 287, 808-813, 2001
A;Title: Expression and characterization of hypoxia-inducible factor (HIF)-3alpha in hum
A;Reference number: JC7771; PMID:11573933
A;Contents: Kidney
A;Accession: JC7771
A;Molecule type: mRNA
A;Residues: 1-667 <HAR>
A;Cross-references: UNIPROT:Q9Y2N7; DDBJ:AB054067
C;Comment: This protein is a heterodimeric transcription factor that belongs to the basi
lved in the regulation of hypoxia-inducible gene expression in human kidney.
C;Genetics:
A;Gene: hif-3alpha
A;Map position: 19
C;Keywords: kidney

Query Match 54.7%; Score 87; DB 2; Length 667;
Best Local Similarity 94.4%; Pred. No. 0.00048;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 LDLEMLAPYIPMDDDFQL 30
|||||||||| |||||||
Db 483 LDLEMLAPYISMDDDFQL 500

RESULT 6
F75370
oligopeptidase A - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75370
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75370
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-685 <WHI>

```
A;Cross-references: UNIPROT:Q9RTU7; GB:AE002008; GB:AE000513; NID:g6459414; PIDN:AAF1121
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1659
A;Map position: 1
C;Superfamily: peptidyl-dipeptidase Dcp

  Query Match             37.1%;  Score 59;  DB 2;  Length 685;
  Best Local Similarity   42.3%;  Pred. No. 3.4;
  Matches   11;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDD 26
              |  :|:|| : | | | | ||  :|:
Db        338 YWAEKQRQEKYDFDEEALRPYFALDN 363


RESULT 7
T09384
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09384
R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir
J. Virol. 69, 4228-4236, 1995
A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon
A;Reference number: Z16654; MUID:95287475; PMID:7769682
A;Accession: T09384
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-71 <MIC>
A;Cross-references: UNIPROT:Q71926; EMBL:U24451; NID:g829440; PIDN:AAA79576.1; PID:g8294
C;Genetics:
A;Gene: tat
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription

  Query Match             36.5%;  Score 58;  DB 2;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              |||||||||||
Db         47 YGRKKRRQRRR 57


RESULT 8
TNLJH4
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 02-Jul-1998
C;Accession: B25523
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: B25523
A;Molecule type: DNA
A;Residues: 1-72 <DES>
A;Cross-references: GB:M13137; NID:g326460
A;Note: the GenBank entry ADRE3AA PID:g209908 differs from the published sequence in tra
C;Genetics:
A;Gene: tat
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription regulation

  Query Match             36.5%;  Score 58;  DB 1;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 0.44;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              |||||||||||
Db         47 YGRKKRRQRRR 57


RESULT 9
TNLJZR
trans-activating transcription regulator - human immunodeficiency virus Zr-6
C;Species: human immunodeficiency virus Zr-6
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: C26192
R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; C
Gene 52, 71-82, 1987
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
A;Reference number: A26192; MUID:87248097; PMID:3036660
A;Accession: C26192
A;Molecule type: DNA
A;Residues: 1-86 <SRI>
A;Cross-references: UNIPROT:P04609; GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45377.1;
C;Genetics:
A;Gene: tat
A;Introns: 72/3
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

  Query Match             36.5%;  Score 58;  DB 1;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              |||||||||||
Db         47 YGRKKRRQRRR 57


RESULT 10
JC5591
transactivator protein - human immunodeficiency virus type 1
N;Alternate names: tat protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C;Accession: JC5591
R;Hoffmann, S.; Willbold, D.
Biochem. Biophys. Res. Commun. 235, 806-811, 1997
A;Title: A selection system to study protein-RNA interactions: Functional display of HI
A;Reference number: JC5591; MUID:97350867; PMID:9207243
A;Accession: JC5591
A;Molecule type: protein
A;Residues: 1-86 <HO2>
C;Comment: This protein is a key regulatory protein in the viral replication cycle and
C;Superfamily: AIDS trans-activating transcription regulator
F;22-31/Region: cysteine-rich

  Query Match             36.5%;  Score 58;  DB 2;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              |||||||||||
Db         47 YGRKKRRQRRR 57


RESULT 11
A25700
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 09-Jul-2004
C;Accession: A25700
R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.
Science 229, 74-77, 1985
A;Reference number: A25700; MUID:85244627; PMID:2990041
A;Accession: A25700
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-86 <SOD>
A;Cross-references: UNIPROT:P04610
C;Superfamily: AIDS trans-activating transcription regulator
```

```
  Query Match             36.5%;  Score 58;  DB 2;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              ||||||||||| 
Db         47 YGRKKRRQRRR 57


RESULT 12
S54381
tat protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54381
R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
A;Accession: S54381
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-86 <THE>
A;Cross-references: UNIPROT:P12506; EMBL:M22639; NID:g329377; PIDN:AAA45363.1; PID:g3293
C;Genetics:
A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator

  Query Match             36.5%;  Score 58;  DB 2;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              ||||||||||| 
Db         47 YGRKKRRQRRR 57


RESULT 13
S33982
trans-activating transcription regulator - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S33982; S26385; S19864
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33982
A;Molecule type: DNA
A;Residues: 1-86 <CAR>
A;Cross-references: UNIPROT:P04606; EMBL:Z11530; NID:g60192; PIDN:CAA77625.1; PID:g60196
R;Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Sumner-Sm
Nucleic Acids Res. 20, 5311-5320, 1992
A;Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator c
A;Reference number: S26385; MUID:93065196; PMID:1437550
A;Accession: S26385
A;Molecule type: nucleic acid
A;Residues: 1-86 <SID>
A;Cross-references: EMBL:X64650; NID:g60144; PIDN:CAA45921.1; PID:g60145
C;Genetics:
A;Gene: tat
A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency

  Query Match             36.5%;  Score 58;  DB 2;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              ||||||||||| 
Db         47 YGRKKRRQRRR 57


RESULT 14
T01665
tat protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01665
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01665
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-87 <ALI>
A;Cross-references: UNIPROT:P04613; EMBL:K03456; NID:g60228; PIDN:CAA28015.1; PID:g60233
C;Genetics:
A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator

  Query Match             36.5%;  Score 58;  DB 2;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 0.53;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              ||||||||||| 
Db         47 YGRKKRRQRRR 57


RESULT 15
TNLJ12
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A04017
R;Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of
A;Reference number: A94093; MUID:86177573; PMID:3008154
A;Accession: A04017
A;Molecule type: DNA
A;Residues: 1-95 <ARY>
A;Cross-references: UNIPROT:P04326
C;Genetics:
A;Gene: tat
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

  Query Match             36.5%;  Score 58;  DB 1;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 0.58;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRR 11
              ||||||||||| 
Db         56 YGRKKRRQRRR 66


RESULT 16
E44001
trans-activating transcription regulator - human immunodeficiency virus type 1 (strain
N;Alternate names: tat protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: E44001
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties o
A;Reference number: A44001; MUID:93021387; PMID:1404605
A;Accession: E44001
A;Molecule type: DNA
A;Residues: 1-101 <LIY>
A;Cross-references: UNIPROT:P35965; GB:M93258
C;Genetics:
```

A;Gene: tat
A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 36.5%; Score 58; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11
||||||||||
Db 47 YGRKKRRQRRR 57

RESULT 17
T09446
tat protein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09446
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09446
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-101 <PAN>
A;Cross-references: UNIPROT:Q75758; EMBL:U63632; NID:g1465777; PID:g1465783
C;Genetics:
A;Gene: tat
A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator

Query Match 36.5%; Score 58; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11
||||||||||
Db 47 YGRKKRRQRRR 57

RESULT 18
TNLJND
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JQ0071
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunc
A;Reference number: JQ0065; MUID:90034200; PMID:2806917
A;Accession: JQ0071
A;Molecule type: DNA
A;Residues: 1-86 <SPI>
A;Cross-references: UNIPROT:P18804; GB:M27323; NID:g328154; PIDN:AAA44866.1; PID:g328155
C;Genetics:
A;Gene: tat
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription

Query Match 34.6%; Score 55; DB 1; Length 86;
Best Local Similarity 90.9%; Pred. No. 1.4;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRR 11
||||||||||:
Db 47 YGRKKRRQRRK 57

RESULT 19
S76766
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76766
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76766
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-713 <KAN>
A;Cross-references: UNIPROT:P74571; EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA186
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Start codon: GTG
C;Superfamily: peptidyl-dipeptidase Dcp

Query Match 34.0%; Score 54; DB 2; Length 713;
Best Local Similarity 37.5%; Pred. No. 17;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAPYIPM 24
| :::|:: | | | | || |:
Db 357 YWSERQREQEFDFDAEALRPYFPL 380

RESULT 20
JC4851
hypoxia-inducible factor 1 alpha homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Accession: JC4851
R;Nambu, J.R.; Chen, W.; Hu, S.; Crews, S.T.
Gene 172, 249-254, 1996
A;Title: The Drosophila melanogaster similar bHLH-PAS gene encodes a protein related to
A;Reference number: JC4851; MUID:96269413; PMID:8682312
A;Accession: JC4851
A;Molecule type: mRNA
A;Residues: 1-1505 <NAM>
A;Cross-references: UNIPROT:Q24167; GB:U43090; NID:g1174073; PIDN:AAC47303.1; PID:g1174
C;Genetics:
A;Gene: sima
A;Cross-references: FlyBase:FBgn0015542
A;Map position: 3
F;72-125/Region: helix-loop-helix #status predicted
F;171-433/Region: PAS domain #status predicted
F;506-635/Region: proline-rich

Query Match 34.0%; Score 54; DB 2; Length 1505;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 17 MLAPYIPMDDDFQL 30
| |||||:||| |
Db 850 MRAPYIPIDDDMPL 863

RESULT 21
B5AG58
virB5 protein precursor - Agrobacterium tumefaciens plasmid pTiC58
C;Species: Agrobacterium tumefaciens
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S12345; S11830; S10520
R;Shirasu, K.; Morel, P.; Kado, C.I.
Mol. Microbiol. 4, 1153-1163, 1990
A;Title: Characterization of the virB operon of an Agrobacterium tumefaciens Ti plasmid
A;Reference number: S12341; MUID:91041724; PMID:2233252
A;Accession: S12345
A;Molecule type: DNA

A;Residues: 1-220 <SHI>
A;Cross-references: UNIPROT:P17795; EMBL:J03320; NID:g154781; PIDN:AAA91595.1; PID:g1547
R;Rogowsky, P.M.; Powell, B.S.; Shirasu, K.; Lin, T.S.; Morel, P.; Zyprian, E.M.; Steck,
Plasmid 23, 85-106, 1990
A;Title: Molecular characterization of the vir regulon of Agrobacterium tumefaciens: com
A;Reference number: S11825; MUID:90301800; PMID:2194232
A;Accession: S11830
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-220 <ROG>
A;Cross-references: EMBL:J03320; NID:g154781; PIDN:AAA91595.1; PID:g154787
R;Kuldau, G.A.; de Vos, G.; Owen, J.; McCaffrey, G.; Zambryski, P.
Mol. Gen. Genet. 221, 256-266, 1990
A;Title: The virB operon of Agrobacterium tumefaciens pTiC58 encodes 11 open reading fra
A;Reference number: S10516; MUID:90318324; PMID:2370849
A;Accession: S10520
A;Molecule type: DNA
A;Residues: 1-220 <KUL>
A;Cross-references: EMBL:X53264; NID:g39152; PIDN:CAA37358.1; PID:g39157
C;Genetics:
A;Gene: virB5
A;Genome: plasmid
C;Superfamily: tumor-inducing plasmid pTiC58 virB5 protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-220/Product: virB5 protein #status predicted <MAT>

Query Match 32.1%; Score 51; DB 1; Length 220;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RKKRRQRRRDLDLEMLAPYIPM 24
:| : |||| || :| :||
Db 72 QKNQYPSTRDLDTEMFSPRMPM 93

RESULT 22
AI3248
component of type IV secretion system [imported] - Agrobacterium tumefaciens (strain C58
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3248
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3248
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KUR>
A;Cross-references: UNIPROT:P17795; GB:AE008690; PIDN:AAL46407.1; PID:g17744201; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: virB5
A;Genome: plasmid
C;Superfamily: tumor-inducing plasmid pTiC58 virB5 protein

Query Match 32.1%; Score 51; DB 2; Length 220;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RKKRRQRRRDLDLEMLAPYIPM 24
:| : |||| || :| :||
Db 72 QKNQYPSTRDLDTEMFSPRMPM 93

RESULT 23
CTXLPA
corticotropin / lipotropin A precursor - African clawed frog
N;Alternate names: POMC; proopiomelanocortin
N;Contains: beta-endorphin; CLIP; corticotropin; lipotropin beta; melanotropin alpha; me
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01460; A42623; S03554; S03555; I51554
R;Martens, G.J.M.
Nucleic Acids Res. 14, 3791-3798, 1986
A;Title: Expression of two proopiomelanocortin genes in the pituitary gland of Xenopus l
A;Reference number: A93621; MUID:86232619; PMID:3754961
A;Accession: A01460
A;Molecule type: mRNA
A;Residues: 1-259 <MAR1>
A;Cross-references: UNIPROT:P06298; GB:X03843; NID:g65004; PIDN:CAA27460.1; PID:g65005
R;Deen, P.M.T.; Bussemakers, M.J.G.; Terwel, D.; Roubos, E.W.; Martens, G.J.M.
Mol. Biol. Evol. 9, 483-494, 1992
A;Title: Comparative structural analysis of the transcriptionally active proopiomelanoco
A;Reference number: A42623; MUID:92261311; PMID:1584015
A;Accession: A42623
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-202,'E',204-259 <DEE>
A;Cross-references: GB:X59370; NID:g5931775; PIDN:CAA42013.2; PID:g5931776
A;Note: this translation is not annotated in GenBank entry XLPOMCA, release 109
R;Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
FEBS Lett. 245, 215-218, 1989
A;Title: Particular processing of pro-opiomelanocortin in Xenopus laevis intermediate pi
A;Reference number: S03554; MUID:89171310; PMID:2564347
A;Accession: S03554
A;Molecule type: protein
A;Residues: 140-149 <ROU1>
A;Note: amino end of melanotropin alpha, which is not acetylated in this preparation
A;Accession: S03555
A;Molecule type: protein
A;Residues: 'X',211-225 <ROU2>
A;Note: amino end of melanotropin beta
R;Martens, G.J.M.; Civelli, O.; Herbert, E.
J. Biol. Chem. 260, 13685-13689, 1985
A;Title: Nucleotide sequence of cloned cDNA for pro-opiomelanocortin in the amphibian Xe
A;Reference number: I51554; MUID:86033833; PMID:3840481
A;Accession: I51554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'L',58-259 <MAR2>
A;Cross-references: GB:M11346; NID:g214659; PIDN:AAA49932.1; PID:g214660
C;Genetics:
A;Introns: 43/3
C;Superfamily: corticotropin-lipotropin
C;Keywords: glycoprotein; hormone; neuropeptide; opioid peptide; pituitary
F;1-25/Domain: signal sequence #status predicted <SIG>
F;76-101/Product: melanotropin gamma #status predicted <MTG>
F;140-178/Product: corticotropin #status predicted <CTN>
F;140-154/Product: melanotropin alpha #status predicted <MTA>
F;157-178/Product: CLIP #status predicted <CLP>
F;181-259/Product: lipotropin beta #status predicted <LTB>
F;210-226/Product: melanotropin beta #status predicted <MTB>
F;229-259/Product: beta-endorphin #status predicted <BEF>
F;229-233/Product: Met-enkephalin #status predicted <MEN>
F;90/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.4%; Score 50; DB 1; Length 259;
Best Local Similarity 28.3%; Pred. No. 21;
Matches 13; Conservative 7; Mismatches 8; Indels 18; Gaps 1;

Qy 2 GRKKR----------RQRRRDLDLEMLAPYIPMDDDFQ 29
|||:| : ||:| ||: | | :|:| :
Db 153 GRKRRPIKVYPNGVEEESAESYPMELRRELSLELDYPEIDLDEDIE 198

RESULT 24
CTXLPB
corticotropin / lipotropin B precursor - African clawed frog
N;Alternate names: gamma-melanocyte stimulating hormone; POMC; pro-opiomelanocortin
N;Contains: beta-endorphin; CLIP; corticotropin; lipotropin beta; melanotropin alpha;
C;Species: Xenopus laevis (African clawed frog)

```
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01461; I51621; S18009; S03554; S03555; I51623; I51624; I51626; I51627; I51
R;Martens, G.J.M.
Nucleic Acids Res. 14, 3791-3798, 1986
A;Title: Expression of two proopiomelanocortin genes in the pituitary gland of Xenopus l
A;Reference number: A93621; MUID:86232619; PMID:3754961
A;Accession: A01461
A;Molecule type: mRNA
A;Residues: 1-260 <MAR1>
A;Cross-references: UNIPROT:P06299; GB:X03844; NID:g65011; PIDN:CAA27466.1; PID:g65012
R;Martens, G.J.
Eur. J. Biochem. 165, 467-472, 1987
A;Title: Structural organization of the proopiomelanocortin gene in Xenopus laevis. 5'-e
A;Reference number: I51621; MUID:87246627; PMID:3595598
A;Accession: I51621
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <MAR2>
A;Cross-references: GB:X05789; NID:g64991; GB:X05941; NID:g64994; GB:X05940; NID:g64992;
R;Deen, P.M.T.; Terwel, D.; Bussemakers, M.J.M.; Roubos, E.W.; Martens, G.J.M.
Eur. J. Biochem. 201, 129-137, 1991
A;Title: Structural analysis of the entire proopiomelanocortin gene of Xenopus laevis.
A;Reference number: S18009; MUID:92007866; PMID:1915355
A;Accession: S18009
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-260 <DEE>
A;Cross-references: EMBL:X59369; NID:g64989; PIDN:CAA42012.1; PID:g64990
R;Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
FEBS Lett. 245, 215-218, 1989
A;Title: Particular processing of pro-opiomelanocortin in Xenopus laevis intermediate pi
A;Reference number: S03554; MUID:89171310; PMID:2564347
A;Accession: S03554
A;Molecule type: protein
A;Residues: 141-150 <ROU1>
A;Note: amino end of melanotropin alpha, which is not acetylated in this preparation
A;Accession: S03555
A;Molecule type: protein
A;Residues: 'X',212-226 <ROU2>
A;Note: amino end of melanotropin beta
C;Genetics:
A;Introns: 43/3
A;Note: the first intron occurs before the initiator codon
C;Superfamily: corticotropin-lipotropin
C;Keywords: glycoprotein; hormone; neuropeptide; opioid peptide; pituitary
F;1-25/Domain: signal sequence #status predicted <SIG>
F;76-101/Product: melanotropin gamma #status predicted <MTG>
F;141-179/Product: corticotropin #status predicted <CTN>
F;141-155/Product: melanotropin alpha #status predicted <MTA>
F;158-179/Product: CLIP #status predicted <CLP>
F;182-260/Product: lipotropin beta #status predicted <LTB>
F;211-227/Product: melanotropin beta #status predicted <MTB>
F;230-260/Product: beta-endorphin #status predicted <BEF>
F;230-234/Product: Met-enkephalin #status predicted <MEN>
F;90/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             31.4%;  Score 50;  DB 1;  Length 260;
  Best Local Similarity   28.3%;  Pred. No. 21;
  Matches   13;  Conservative    7;  Mismatches    8;  Indels   18;  Gaps    1;

Qy          2 GRKKR-----------------RQRRRDLDLEMLAPYIPMDDDFQ 29
              |||:|                 : ||:| ||:  | | :|:| :
Db        154 GRKRRPIKVYPNGVEEESAESFPMELRRELSLELDYPEIDLDEDIE 199


RESULT 25
B38965
hypothetical protein B - Enterobacter agglomerans insertion sequence IS1222
C;Species: Enterobacter agglomerans
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: B38965; S42922
R;Steibl, H.D.; Lewecke, F.M.
Gene 156, 37-42, 1995
A;Title: IS1222: analysis and distribution of a new insertion sequence in Enterobacter a
A;Reference number: A38965; MUID:95255664; PMID:7737514
A;Accession: B38965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <STE>
A;Cross-references: UNIPROT:Q46612; GB:X78052; NID:g459246; PIDN:CAA54973.1; PID:g459248
A;Experimental source: strain Kleeberger, 1983
C;Genetics:
A;Mobile element: insertion sequence IS1222

  Query Match             31.4%;  Score 50;  DB 2;  Length 276;
  Best Local Similarity   43.3%;  Pred. No. 22;
  Matches   13;  Conservative    3;  Mismatches    8;  Indels    6;  Gaps    1;

Qy          5 KRRQRRRDLDLEML------APYIPMDDDF 28
              |||:||: |  | |       || :   |||
Db         85 KRRRRRKGLATERLPLLRPAAPNLTWSDDF 114


RESULT 26
D83741
hypothetical protein BH0732 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83741
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83741
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-457 <STO>
A;Cross-references: UNIPROT:Q9KEW7; GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB044
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0732

  Query Match             31.4%;  Score 50;  DB 2;  Length 457;
  Best Local Similarity   40.0%;  Pred. No. 38;
  Matches   10;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          2 GRKKRRQRRRDLDLEMLAPYIPMDD 26
              |:|  |: |   :|  :  ||| ||
Db        202 GKKVNRKERTGSELHAIREYIPDDD 226


RESULT 27
E70610
hypothetical protein Rv1215c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70610
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70610
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-561 <COL>
A;Cross-references: UNIPROT:O05316; GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07817.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1215c

  Query Match             31.4%;  Score 50;  DB 2;  Length 561;
  Best Local Similarity   35.7%;  Pred. No. 47;
  Matches   10;  Conservative    6;  Mismatches   12;  Indels    0;  Gaps    0;
```

```
Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDF 28
              : |  ||: |:  |:| :    |: |||
Db        229 WSRGVRRRTRQTYDMEQMQEAHPLRDDF 256
```

RESULT 28
T01773
syntaxin homolog A_IG002P16.16 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
C;Accession: T01773
R;Miller, N.; Beck, C.; Kramer, J.
submitted to the EMBL Data Library, June 1997
A;Description: The sequence of A. thaliana IG002P16.
A;Reference number: Z14421
A;Accession: T01773
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-307 <MIL>
A;Cross-references: EMBL:AF007270; NID:g2191157; PID:g2191179
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 5
A;Introns: 67/2; 159/3; 189/3; 213/3; 249/3; 271/3
A;Note: A_IG002P16.16

  Query Match 31.1%; Score 49.5; DB 2; Length 307;
  Best Local Similarity 38.7%; Pred. No. 29;
  Matches 12; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

```
Qy          1 YGRKKRRQRRRDLDLEMLAP---YIPMDDDF 28
              | :: |:|:   :||||      | | :|||
Db        180 YLKRLRQQKEDGMDLEMNLSRNRYRPEEDDF 210
```

RESULT 29
F64651
hypothetical protein HP1054 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: F64651
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64651
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-422 <TOM>
A;Cross-references: UNIPROT:O25694; GB:AE000613; GB:AE000511; NID:g2314200; PIDN:AAD0810
C;Genetics:
A;Start codon: TTG

  Query Match 30.8%; Score 49; DB 2; Length 422;
  Best Local Similarity 37.9%; Pred. No. 47;
  Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQ 29
              : ||  | | :|:||  |   |   : ||
Db        215 FKRKIHRLREKDIDLSALKDKIAKQEKFQ 243
```

RESULT 30
G71939
hypothetical protein jhp0371 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71939
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71939
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 <ARN>
A;Cross-references: UNIPROT:Q9ZM52; GB:AE001472; GB:AE001439; NID:g4154897; PIDN:AAD0595
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0371

  Query Match 30.8%; Score 49; DB 2; Length 440;
  Best Local Similarity 37.9%; Pred. No. 50;
  Matches 11; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQ 29
              : ||  | | ||:|  |   |   : ||
Db        233 FKRKTHRLRERDINLSALKDKIAKQEKFQ 261
```

RESULT 31
B70694
probable infB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70694
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70694
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-900 <COL>
A;Cross-references: UNIPROT:P71613; GB:Z81331; GB:AL123456; NID:g3261650; PIDN:CAB03670
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo
C;Keywords: GTP binding; nucleotide binding; P-loop
F;399-512/Domain: translation elongation factor Tu homology <ETU>
F;405-412/Region: nucleotide-binding motif A (P-loop)
F;509-512/Region: GTP-binding NKXD motif
F;545-547/Region: GTP-binding SAK/L motif
F;411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #

  Query Match 30.5%; Score 48.5; DB 2; Length 900;
  Best Local Similarity 47.6%; Pred. No. 1.2e+02;
  Matches 10; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```
Qy          2 GRKKRRQRRRDLDLEMLAPYI 22
              ||| :||:|:: |  | || :
Db        277 GRKSKRQKRQEYD-SMQAPVV 296
```

RESULT 32
F87103
initiation factor IF-2 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87103
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.

```
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F87103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <STO>
A;Cross-references: UNIPROT:Q9Z5I9; GB:AL450380; NID:g13093370; PIDN:CAC30507.1; GSPDB:G
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo

  Query Match             30.5%;  Score 48.5;  DB 2;  Length 924;
  Best Local Similarity   47.6%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          2 GRKKRRQRRRDLDLEMLAPYI 22
              ||| :||:|:: |  | || :
Db        301 GRKSKRQKRQEYD-SMQAPVV 320


RESULT 33
A70966
hypothetical protein Rv2653c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70966
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70966
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <COL>
A;Cross-references: UNIPROT:P71950; GB:Z80225; GB:AL123456; NID:g3242265; PIDN:CAB02358.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2653c
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2653c

  Query Match             30.2%;  Score 48;  DB 2;  Length 107;
  Best Local Similarity   40.0%;  Pred. No. 15;
  Matches   12;  Conservative    6;  Mismatches    6;  Indels    6;  Gaps    1;

Qy          4 KKRRQRRRDLD------LEMLAPYIPMDDD 27
              ::| ||:|||:       ||:|    :|||
Db         39 QRRAQRQRDLEAIRRAYAEMVATSHEIDDD 68


RESULT 34
D71218
hypothetical protein PH0007 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: D71218
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71218
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-232 <KAW>
A;Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29075.1; PID:g3256392
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0007
C;Superfamily: nucleotidyltransferase

  Query Match             30.2%;  Score 48;  DB 2;  Length 232;
  Best Local Similarity   42.9%;  Pred. No. 35;
  Matches    9;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAPY 21
              ||   |   ||| |:::: ||
Db         47 YGSVARGDVRRDSDIDIVIPY 67


RESULT 35
D75185
hypothetical protein PAB0004 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 12-Jun-2003
C;Accession: D75185
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A;Reference number: A75001
A;Accession: D75185
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <KAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB48931.1; PID:g545744
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0004
C;Superfamily: nucleotidyltransferase

  Query Match             30.2%;  Score 48;  DB 2;  Length 233;
  Best Local Similarity   42.9%;  Pred. No. 35;
  Matches    9;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAPY 21
              ||   |   ||| |:::: ||
Db         48 YGSVARGDVRRDSDIDIVIPY 68


RESULT 36
S35637
high mobility group 1 protein homolog - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: S35637; S35636; I84754
R;Wang, L.; Precht, P.; Balakir, R.; Horton Jr., W.E.
submitted to the EMBL Data Library, January 1993
A;Reference number: S35637
A;Accession: S35637
A;Molecule type: mRNA
A;Residues: 1-561 <WAN>
A;Cross-references: UNIPROT:Q04931; GB:L08814; NID:g203464; PIDN:AAA40927.1; PID:g203465
R;Wang, L.; Precht, P.; Balakir, R.; Horton Jr., W.E.
Nucleic Acids Res. 21, 1493, 1993
A;Title: Rat and chick cDNA clones encoding HMG-like proteins.
A;Reference number: I50198; MUID:93219134; PMID:8464746
A;Accession: S35636
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 391-476 <WAW>
A;Cross-references: GB:L08814; NID:g203464; PIDN:AAA40927.1; PID:g203465
C;Genetics:
A;Gene: CIIDBP
C;Superfamily: HMG box homology
C;Keywords: DNA binding
F;396-471/Domain: HMG box homology <HMG1>

  Query Match             30.2%;  Score 48;  DB 2;  Length 561;
  Best Local Similarity   45.8%;  Pred. No. 88;
  Matches   11;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 KKRRQRRRDLDLEMLAPYIPMDDD 27
              ||:|:|  | | | ||   |  :|
Db        531 KKKRRRSEDSDEEELASTPPSSED 554
```

RESULT 37
S41218
HIR1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBL008w; protein YBL0318
C;Species: Saccharomyces cerevisiae
C;Date: 28-Jan-1994 #sequence_revision 09-Sep-1994 #text_change 16-Aug-2004
C;Accession: S41218; S45741; S33389; S38776
R;Delaveau, T.; Jacq, C.; Perea, J.
Yeast 8, 761-768, 1992
A;Title: Sequence of a 12.7 kb segment of yeast chromosome II identifies a PDR-like gene
A;Reference number: S25326; MUID:93070613; PMID:1441753
A;Accession: S41218
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-840 <DEL>
A;Cross-references: UNIPROT:P32479; EMBL:S47695; NID:g259049; PIDN:AAB23989.1; PID:g1680
A;Experimental source: strain S288C
R;Delaveau, T.; Jacq, C.; Perea, J.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45736
A;Accession: S45741
A;Molecule type: DNA
A;Residues: 1-840 <DE2>
A;Cross-references: EMBL:Z35769; NID:g535991; PIDN:CAA84827.1; PID:g535992; MIPS:YBL008w
A;Experimental source: strain S288C
R;Sherwood, P.W.; Tsang, S.V.M.; Osley, M.A.
Mol. Cell. Biol. 13, 28-38, 1993
A;Title: Characterization of HIR1 and HIR2, two genes required for regulation of histone
A;Reference number: S33389; MUID:93109312; PMID:8417331
A;Accession: S33389
A;Molecule type: DNA
A;Residues: 53-259,'V',261-339,'M',341-840 <SHE>
A;Cross-references: EMBL:L03838
R;Sherwood, P.W.; Tsang, S.V.; Osley, M.A.
submitted to the EMBL Data Library, October 1992
A;Reference number: S38776
A;Accession: S38776
A;Molecule type: DNA
A;Residues: 53-242,'MGNILQFRTPLM',255-259,'V',261-339,'M',341-840 <SH2>
A;Cross-references: EMBL:L03838
C;Genetics:
A;Gene: SGD:HIR1
A;Cross-references: SGD:S0000104; MIPS:YBL008w
A;Map position: 2L
C;Superfamily: WD repeat homology
C;Keywords: nucleus; transcription regulation
F;75-108/Domain: WD repeat homology <WD1>
F;133-166/Domain: WD repeat homology <WD2>
F;352-385/Domain: WD repeat homology <WD5>

Query Match 30.2%; Score 48; DB 2; Length 840;
Best Local Similarity 45.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 11 RDLDLEMLAPYIPMDDDFQL 30
|::|| | | ||: | |:
Db 51 RCMELESLTPEIPLPQDLQM 70

RESULT 38
A28199
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004
C;Accession: A28199
R;Takeyasu, K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.
J. Biol. Chem. 263, 4347-4354, 1988
A;Title: Ouabain-sensitive (Na(+) + K(+))-ATPase activity expressed in mouse L cells by
A;Reference number: A28199; MUID:88153759; PMID:2831227
A;Accession: A28199
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1021 <TAK>
A;Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211220
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F;585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F;213,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;506/Binding site: ATP (Lys) #status predicted

Query Match 30.2%; Score 48; DB 2; Length 1021;
Best Local Similarity 42.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 1 YGRKKRRQRRRDLDLEMLAPYIPMDD 26
:| ||:: : ||:| | | |||
Db 18 HGTKKKKAKERDMD--ELKKEISMDD 41

RESULT 39
A24639
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] - rat
N;Alternate names: Na+/K+-transporting ATPase alpha chain, kidney-type
N;Contains: Na+/K+-transporting ATPase alpha-S chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758
R;Shull, G.E.; Greeb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986
A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit fr
A;Reference number: A90512; MUID:87128908; PMID:3028470
A;Accession: A24639
A;Molecule type: mRNA
A;Residues: 1-1023 <SHU>
A;Cross-references: UNIPROT:P06685; EMBL:M14511; NID:g203026; PIDN:AAA40775.1; PID:g2030
R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; N
J. Biochem. 102, 43-58, 1987
A;Title: Primary structures of two types of alpha-subunit of rat brain Na(+),K(+)-ATPase
A;Reference number: S00460; MUID:88032933; PMID:2822682
A;Accession: S00460
A;Molecule type: mRNA
A;Residues: 1-1023 <HAR>
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
J. Cell Biol. 105, 1855-1865, 1987
A;Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: structural a
A;Reference number: A92749; MUID:88033255; PMID:2822726
A;Accession: A27180
A;Molecule type: mRNA
A;Residues: 1-67,'PV',70-174,'E',176-187,'V',189-334,'V',336-1023 <HER>
A;Cross-references: EMBL:M28647; NID:g205631; PIDN:AAA41671.1; PID:g205632
R;Yagawa, Y.; Kawakami, K.; Nagano, K.
Biochim. Biophys. Acta 1049, 286-292, 1990
A;Title: Cloning and analysis of the 5'-flanking region of rat Na(+)/K(+)-ATPase alpha-1
A;Reference number: S11020; MUID:90344872; PMID:2166579
A;Accession: S11020
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-41 <YAG>
A;Cross-references: EMBL:X53233
R;Schneider, J.W.; Mercer, R.W.; Caplan, M.; Emanuel, J.R.; Sweadner, K.J.; Benz Jr., E
Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985
A;Title: Molecular cloning of rat brain Na,K-ATPase alpha-subunit cDNA.
A;Reference number: A25171; MUID:85298352; PMID:2994074
A;Accession: A25171
A;Molecule type: mRNA
A;Residues: 489-533 <SCH>
R;Lytton, J.
Biochem. Biophys. Res. Commun. 132, 764-769, 1985
A;Title: The catalytic subunits of the (Na(+), K(+))-ATPase alpha and alpha(+) isozymes
A;Reference number: S29877; MUID:86050667; PMID:2998384
A;Accession: S29877
A;Status: preliminary

A;Molecule type: protein
A;Residues: 6-19 <LYT>
R;Kurihara, K.; Hosoi, K.; Kodama, A.; Ueha, T.
Biochim. Biophys. Acta 1039, 234-240, 1990
A;Title: A new electrophoretic variant of alpha subunit of Na(+)/K(+)-ATPase from the su
A;Reference number: S10758; MUID:90304196; PMID:2163680
A;Accession: S10758
A;Molecule type: protein
A;Residues: 6,'X',8-10,'X',12-16 <KUR>
A;Experimental source: submandibular gland
A;Note: designated alpha-S form; thought to arise from alpha-1 chain by post-translation
C;Genetics:
A;Gene: NKAA1
A;Introns: 4/3
A;Note: the list of introns may be incomplete
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status experimental <MAT>
F;6-95/Domain: intracellular #status predicted <INT1>
F;96-120/Domain: transmembrane #status predicted <TM1>
F;130-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <INT2>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;349-786/Domain: intracellular #status predicted <INT3>
F;587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F;787-810/Domain: transmembrane #status predicted <TM5>
F;849-874/Domain: transmembrane #status predicted <TM6>
F;875-952/Domain: intracellular #status predicted <INT4>
F;953-978/Domain: transmembrane #status predicted <TM7>
F;979-1023/Domain: extracellular #status predicted <EXT>
F;376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;508/Binding site: ATP (Lys) #status predicted
F;717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 30.2%; Score 48; DB 1; Length 1023;
Best Local Similarity 30.8%; Pred. No. 1.6e+02;
Matches 8; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 YGRKKRRQRRRDLDLEMLAPYIPMDD 26
              :| || :: ::: |:: |   : |||
Db         18 HGDKKSKKAKKERDMDELKKEVSMDD 43
```

RESULT 40
A24414
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human
N;Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain
C;Species: Homo sapiens (man)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24414; A27795; A39910; I60116; S09171
R;Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.
J. Biochem. 100, 389-397, 1986
A;Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA s
A;Reference number: A24414; MUID:87057096; PMID:2430951
A;Accession: A24414
A;Molecule type: mRNA
A;Residues: 1-1023 <KAW>
A;Cross-references: UNIPROT:P05023; EMBL:X04297; NID:g28926; PIDN:CAA27840.1; PID:g28927
R;Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A;Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.
A;Reference number: A94158; MUID:87231946; PMID:3035563
A;Accession: A27795
A;Molecule type: DNA
A;Residues: 168-189;213-214,'X',216-244 <SHU>
R;Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
A;Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, D
A;Reference number: A39910; MUID:88068506; PMID:2891135
A;Accession: A39910
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 199-942 <CHE>
A;Cross-references: GB:J03007
R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
Genomics 6, 451-460, 1990
A;Title: The human Na, K-ATPase alpha 1 gene: characterization of the 5'-flanking regio
A;Reference number: I60116; MUID:90228961; PMID:1970326
A;Accession: I60116
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-61 <RES>
A;Cross-references: GB:M30310; NID:g179206; PIDN:AAA51801.1; PID:g179208
C;Genetics:
A;Gene: GDB:ATP1A1
A;Cross-references: GDB:119711; OMIM:182310
A;Map position: 1p13-1p11
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
F;6-95/Domain: intracellular #status predicted <INT1>
F;96-120/Domain: transmembrane #status predicted <TM1>
F;130-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <INT2>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;349-786/Domain: intracellular #status predicted <INT3>
F;587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F;787-810/Domain: transmembrane #status predicted <TM5>
F;849-874/Domain: transmembrane #status predicted <TM6>
F;875-952/Domain: intracellular #status predicted <INT4>
F;953-978/Domain: transmembrane #status predicted <TM7>
F;979-1023/Domain: extracellular #status predicted <EXT>
F;376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;508/Binding site: ATP (Lys) #status predicted
F;717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 30.2%; Score 48; DB 2; Length 1023;
Best Local Similarity 36.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```
Qy          2 GRKKRRQRRRDLDLEMLAPYIPMDD 26
              | || :: ::| |:: |   : |||
Db         19 GDKKGKKGKKDRDMDELKKEVSMDD 43
```

RESULT 41
T13855
suppressor of sable protein homolog - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13855
R;Steinhauer, W.R.; Sterling, J.F.; Graves, J.P.
submitted to the EMBL Data Library, February 1995
A;Description: Comparison of suppressor of sable [su(s)] in two Drosphila species reveal
A;Reference number: Z14224
A;Accession: T13855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1473 <STE>
A;Cross-references: UNIPROT:Q24707; EMBL:U20660; NID:g671707; PID:g671708; PIDN:AAA6230
C;Genetics:
A;Cross-references: FlyBase:FBgn0013921
A;Introns: 112/1; 216/3; 702/2; 735/1

Query Match 30.2%; Score 48; DB 2; Length 1473;
Best Local Similarity 40.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

```
Qy          3 RKKRRQRRRDLDLEMLAPYIPM 24
              |    :| || |::|  |: ||
Db        976 RASAAKRERDRDIDMRLPFEPM 997
```

RESULT 42

```
T37242
transforming growth factor beta unc-129 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37242
R;Colavita, A.; Krishna, S.; Zheng, H.; Padgett, R.W.; Culotti, J.G.
Science 281, 706-709, 1998
A;Title: Pioneer axon guidance by UNC-129, a C. elegans TGF-beta.
A;Reference number: Z21640; MUID:98350209; PMID:9685266
A;Accession: T37242
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-407 <COL>
A;Cross-references: UNIPROT:O44371; EMBL:AF029887; NID:g2731819; PIDN:AAC48376.1; PID:g2
A;Experimental source: strain N2
C;Genetics:
A;Gene: unc-129
A;Map position: IV
C;Function:
A;Description: involved in axonal guidance and guided cell migrations

  Query Match             29.9%;  Score 47.5;  DB 2;  Length 407;
  Best Local Similarity   37.9%;  Pred. No. 73;
  Matches   11;  Conservative    7;  Mismatches    6;  Indels    5;  Gaps    1;

Qy          4 KKRRQRRRDLDLEMLAPY-----IPMDDD 27
              :: :::|||| | | |     ||:|:|
Db        224 EQTKRKRRDLGNEELREYYNYNSIPLDND 252


RESULT 43
C85651
hypothetical protein Z1556 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85651
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85651
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <STO>
A;Cross-references: UNIPROT:Q8XAK4; GB:AE005174; NID:g12514427; PIDN:AAG55671.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1556

  Query Match             29.9%;  Score 47.5;  DB 2;  Length 462;
  Best Local Similarity   37.9%;  Pred. No. 84;
  Matches   11;  Conservative    5;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRDLD-LEMLAPYIPMDDDF 28
              | | ::||:|  :| |     | |:|  |
Db        330 YSRAEQRQQRELIDFLNTTTGYAPLDQAF 358


RESULT 44
H90790
hypothetical protein ECs1296 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90790
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <HAY>
A;Cross-references: UNIPROT:Q8XAK4; GB:BA000007; PIDN:BAB34719.1; PID:g13360756; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1296

  Query Match             29.9%;  Score 47.5;  DB 2;  Length 462;
  Best Local Similarity   37.9%;  Pred. No. 84;
  Matches   11;  Conservative    5;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRDLD-LEMLAPYIPMDDDF 28
              | | ::||:|  :| |     | |:|  |
Db        330 YSRAEQRQQRELIDFLNTTTGYAPLDQAF 358


RESULT 45
T20192
hypothetical protein C53D6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20192
R;Gardner, A.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19235
A;Accession: T20192
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-563 <WIL>
A;Cross-references: EMBL:Z70270; PIDN:CAA94230.1; GSPDB:GN00022; CESP:C53D6.2
A;Experimental source: clone C53D6
C;Genetics:
A;Gene: CESP:C53D6.2
A;Map position: 4
A;Introns: 42/1; 62/3; 310/3; 385/2; 406/1; 412/1; 464/3; 529/1

  Query Match             29.9%;  Score 47.5;  DB 2;  Length 563;
  Best Local Similarity   37.9%;  Pred. No. 1e+02;
  Matches   11;  Conservative    7;  Mismatches    6;  Indels    5;  Gaps    1;

Qy          4 KKRRQRRRDLDLEMLAPY-----IPMDDD 27
              :: :::|||| | | |     ||:|:|
Db        224 EQTKRKRRDLGNEELREYYNYNSIPLDND 252


RESULT 46
S74207
lipoxygenase (EC 1.13.11.12) - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: S74207; S74137
R;Hoehne, M.; Nellen, A.; Schwennesen, K.; Kindl, H.
Eur. J. Biochem. 241, 6-11, 1996
A;Title: Lipid body lipoxygenase characterized by protein fragmentation, cDNA sequence
A;Reference number: S74137; MUID:97054584; PMID:8898881
A;Accession: S74207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-878 <HOE>
A;Cross-references: UNIPROT:Q42710; EMBL:X92890; NID:g1296511; PIDN:CAA63483.1
A;Experimental source: tissue cotyledones; clone pCSLBLOX221
A;Accession: S74137
A;Molecule type: protein
A;Residues: 196,'X',198-204;218,'FX',221-223,'XX',226-228;305-309,'XX',312-316;441-460;8
C;Superfamily: lipoxygenase
C;Keywords: oxidoreductase

  Query Match             29.9%;  Score 47.5;  DB 2;  Length 878;
  Best Local Similarity   38.2%;  Pred. No. 1.6e+02;
  Matches   13;  Conservative    6;  Mismatches    8;  Indels    7;  Gaps    2;

Qy          2 GRKKRRQRRRDLDLE-MLAP------YIPMDDDF 28
              || | : ||| : |  |:|       |:| |::|
Db        251 GRTGRPRSRRDHNYESRLSPIMSLDIYVPKDENF 284
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RESULT 47
G64139
DNA-directed RNA polymerase (EC 2.7.7.6) omega chain - Haemophilus influenzae (strain Rd
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: G64139
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64139
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-88 <TIGR>
A;Cross-references: UNIPROT:P43740; GB:U32848; GB:L42023; NID:g3212240; PIDN:AAC23389.1;
C;Superfamily: DNA-directed RNA polymerase omega chain
C;Keywords: nucleotidyltransferase; RNA biosynthesis; transcription

  Query Match 29.6%; Score 47; DB 2; Length 88;
  Best Local Similarity 45.0%; Pred. No. 17;
  Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 8 QRRRDLDLEMLAPYIPMDDD 27
:| | | | || :| |:|
Db 25 RRARQLQLNQSAPLVPEDND 44

RESULT 48
B82444
hypothetical protein VCA0561 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82444
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82444
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <HEI>
A;Cross-references: UNIPROT:Q9KM28; GB:AE004387; GB:AE003853; NID:g9657967; PIDN:AAF9646
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0561
A;Map position: 2

  Query Match 29.6%; Score 47; DB 2; Length 124;
  Best Local Similarity 37.5%; Pred. No. 25;
  Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 7 RQRRRDLDLEMLAPYIPMDDDFQL 30
|:| || |: :: : ||| :|
Db 86 RRRNRDSDVPVIFTHARFDDDAEL 109

RESULT 49
A81971
lacto-N-neotetraose biosynthesis glycosyl transferase NMA0525 [imported] - Neisseria men
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A81971
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81971
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <PAR>
A;Cross-references: UNIPROT:P57033; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB8381
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: lgtB; NMA0525
C;Superfamily: lipopolysaccharide biosynthesis-associated protein

  Query Match 29.6%; Score 47; DB 2; Length 279;
  Best Local Similarity 47.4%; Pred. No. 58;
  Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RKKRRQRRRDLDLEMLAPY 21
|:|||||| | ::: |:
Db 260 REKRRQRREQLIGKIIVPF 278

RESULT 50
I49585
CD2 antigen protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49585
R;Yagita, H.; Okumura, K.; Nakauchi, H.
J. Immunol. 140, 1321-1326, 1988
A;Title: Molecular cloning of the murine homologue of CD2: Homology of the molecule to i
A;Reference number: I49585; MUID:88140313; PMID:3257775
A;Accession: I49585
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <RES>
A;Cross-references: UNIPROT:P08920; GB:M18934; NID:g192486; PIDN:AAA37397.1; PID:g309158
C;Superfamily: T-cell surface glycoprotein CD2

  Query Match 29.6%; Score 47; DB 2; Length 344;
  Best Local Similarity 52.9%; Pred. No. 72;
  Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RKKRRQRRRDLDLEMLA 19
|:|| :||:| :||: |
Db 231 RRKRNRRRKDEELEIKA 247

Search completed: February 9, 2005, 05:57:35
Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 8, 2005, 20:10:07 ; Search time 43.6842 Seconds
(without alignments)
51.265 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 153
Sequence: 1 YGRKKRRQRRRDLDLEMLAXYIPMDDDFQL 30

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	95	62.1	19	4	US-09-959-873B-8	Sequence 8, Appli
2	95	62.1	34	4	US-09-959-873B-9	Sequence 9, Appli
3	95	62.1	54	4	US-09-438-833-13	Sequence 13, Appl
4	95	62.1	116	4	US-09-438-833-8	Sequence 8, Appli
5	95	62.1	288	4	US-09-438-833-9	Sequence 9, Appli
6	95	62.1	301	4	US-09-438-833-10	Sequence 10, Appl
7	95	62.1	311	4	US-09-438-833-7	Sequence 7, Appli
8	95	62.1	532	4	US-09-949-016-7389	Sequence 7389, Ap
9	95	62.1	613	4	US-09-438-833-6	Sequence 6, Appli
10	95	62.1	652	4	US-09-438-833-5	Sequence 5, Appli
11	95	62.1	756	4	US-09-438-833-11	Sequence 11, Appl
12	95	62.1	805	2	US-08-480-473B-4	Sequence 4, Appli
13	95	62.1	805	3	US-08-915-213-4	Sequence 4, Appli
14	95	62.1	805	3	US-09-235-217-4	Sequence 4, Appli
15	95	62.1	805	5	PCT-US96-10251-4	Sequence 4, Appli
16	95	62.1	810	1	US-08-785-241-7	Sequence 7, Appli
17	95	62.1	813	4	US-09-438-833-12	Sequence 12, Appl
18	95	62.1	826	1	US-08-785-241-6	Sequence 6, Appli
19	95	62.1	826	2	US-08-480-473B-2	Sequence 2, Appli
20	95	62.1	826	3	US-08-915-213-2	Sequence 2, Appli
21	95	62.1	826	3	US-09-148-547-2	Sequence 2, Appli
22	95	62.1	826	3	US-09-235-217-2	Sequence 2, Appli
23	95	62.1	826	3	US-09-380-662-23	Sequence 23, Appl
24	95	62.1	826	4	US-09-438-833-1	Sequence 1, Appli
25	95	62.1	826	4	US-09-702-705-330	Sequence 330, App
26	95	62.1	826	4	US-09-736-457-330	Sequence 330, App
27	95	62.1	826	4	US-09-383-581-2	Sequence 2, Appli
28	95	62.1	826	4	US-09-614-124B-330	Sequence 330, App
29	95	62.1	826	4	US-09-671-325-330	Sequence 330, App
30	95	62.1	826	4	US-09-589-184-330	Sequence 330, App
31	95	62.1	826	4	US-09-658-824-330	Sequence 330, App
32	95	62.1	826	4	US-09-959-873B-18	Sequence 18, Appl
33	95	62.1	826	4	US-09-949-016-6089	Sequence 6089, Ap
34	95	62.1	826	4	US-09-967-388-4	Sequence 4, Appli
35	95	62.1	826	5	PCT-US96-10251-2	Sequence 2, Appli
36	95	62.1	827	4	US-09-919-039-149	Sequence 149, App
37	83	54.2	19	4	US-09-972-784-5	Sequence 5, Appli
38	70.5	46.1	205	3	US-09-374-454-2	Sequence 2, Appli
39	70.5	46.1	870	1	US-08-785-241-4	Sequence 4, Appli
40	70.5	46.1	870	3	US-09-374-454-6	Sequence 6, Appli
41	70.5	46.1	875	1	US-08-785-241-5	Sequence 5, Appli
42	69	45.1	385	1	US-08-450-257-58	Sequence 58, Appl
43	69	45.1	385	1	US-08-450-246-58	Sequence 58, Appl
44	69	45.1	385	1	US-08-450-098-58	Sequence 58, Appl
45	69	45.1	385	1	US-08-451-233-58	Sequence 58, Appl
46	69	45.1	385	1	US-08-450-236-58	Sequence 58, Appl
47	69	45.1	385	3	US-08-235-403-58	Sequence 58, Appl
48	63	41.2	32	2	US-08-706-741B-87	Sequence 87, Appl
49	63	41.2	32	2	US-08-924-695A-87	Sequence 87, Appl
50	60	39.2	28	3	US-09-041-886-50	Sequence 50, Appl
51	60	39.2	28	3	US-09-041-886-56	Sequence 56, Appl
52	60	39.2	134	1	US-08-450-257-38	Sequence 38, Appl
53	60	39.2	134	1	US-08-450-246-38	Sequence 38, Appl
54	60	39.2	134	1	US-08-450-098-38	Sequence 38, Appl
55	60	39.2	134	1	US-08-451-233-38	Sequence 38, Appl
56	60	39.2	134	1	US-08-450-236-38	Sequence 38, Appl
57	60	39.2	134	3	US-08-235-403-38	Sequence 38, Appl
58	60	39.2	143	1	US-08-450-257-63	Sequence 63, Appl
59	60	39.2	143	1	US-08-450-246-63	Sequence 63, Appl
60	60	39.2	143	1	US-08-450-098-63	Sequence 63, Appl
61	60	39.2	143	1	US-08-451-233-63	Sequence 63, Appl
62	60	39.2	143	1	US-08-450-236-63	Sequence 63, Appl
63	60	39.2	143	3	US-08-235-403-63	Sequence 63, Appl
64	58	37.9	11	2	US-08-706-741B-54	Sequence 54, Appl
65	58	37.9	11	2	US-08-924-695A-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-959-873B-8
; Sequence 8, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-09-959-873B-8

Query Match 62.1%; Score 95; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.2e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 DLDLEMLAXYIPMDDDFQL 30
               ||||||||:||||||||||
Db           1 DLDLEMLAPYIPMDDDFQL 19
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RESULT 2
US-09-959-873B-9
; Sequence 9, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-959-873B-9

Query Match 62.1%; Score 95; DB 4; Length 34;
Best Local Similarity 94.7%; Pred. No. 4.4e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 DLDLEMLAXYIPMDDDFQL 30
               ||||||||:||||||||||
Db           8 DLDLEMLAPYIPMDDDFQL 26
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RESULT 3
US-09-438-833-13
; Sequence 13, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 531-584 of human HIF-1 alpha
US-09-438-833-13

Query Match 62.1%; Score 95; DB 4; Length 54;
Best Local Similarity 94.7%; Pred. No. 7.7e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 DLDLEMLAXYIPMDDDFQL 30
               ||||||||:||||||||||
Db          26 DLDLEMLAPYIPMDDDFQL 44
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RESULT 4
US-09-438-833-8
; Sequence 8, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-641 of human HIF-1 alpha
US-09-438-833-8

Query Match 62.1%; Score 95; DB 4; Length 116;
Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 DLDLEMLAXYIPMDDDFQL 30
               ||||||||:||||||||||
Db          31 DLDLEMLAPYIPMDDDFQL 49
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RESULT 5
US-09-438-833-9
; Sequence 9, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-813 of human HIF-1 alpha
US-09-438-833-9

Query Match 62.1%; Score 95; DB 4; Length 288;
Best Local Similarity 94.7%; Pred. No. 5.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 DLDLEMLAXYIPMDDDFQL 30
               ||||||||:||||||||||
Db          31 DLDLEMLAPYIPMDDDFQL 49
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RESULT 6
US-09-438-833-10
; Sequence 10, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-826 of human HIF-1 alpha
US-09-438-833-10

Query Match 62.1%; Score 95; DB 4; Length 301;
Best Local Similarity 94.7%; Pred. No. 5.9e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 7
US-09-438-833-7
; Sequence 7, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 331-641 of human HIF-1 alpha
US-09-438-833-7

Query Match 62.1%; Score 95; DB 4; Length 311;
Best Local Similarity 94.7%; Pred. No. 6.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 226 DLDLEMLAPYIPMDDDFQL 244

RESULT 8
US-09-949-016-7389
; Sequence 7389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7389
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7389

Query Match 62.1%; Score 95; DB 4; Length 532;
Best Local Similarity 94.7%; Pred. No. 1.2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 262 DLDLEMLAPYIPMDDDFQL 280

RESULT 9
US-09-438-833-6
; Sequence 6, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-438-833-6

Query Match 62.1%; Score 95; DB 4; Length 613;
Best Local Similarity 94.7%; Pred. No. 1.4e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 343 DLDLEMLAPYIPMDDDFQL 361

RESULT 10
US-09-438-833-5
; Sequence 5, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 1-652 of human HIF-1 alpha
US-09-438-833-5

Query Match 62.1%; Score 95; DB 4; Length 652;
Best Local Similarity 94.7%; Pred. No. 1.5e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 11
US-09-438-833-11
; Sequence 11, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants

```
;  FILE REFERENCE: 1848
;  CURRENT APPLICATION NUMBER: US/09/438,833
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 756
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Subdomain
;   OTHER INFORMATION: 71-826 of human HIF-1 alpha
US-09-438-833-11

  Query Match             62.1%;  Score 95;  DB 4;  Length 756;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        486 DLDLEMLAPYIPMDDDFQL 504


RESULT 12
US-08-480-473B-4
; Sequence 4, Application US/08480473B
; Patent No. 5882914
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,473B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  805 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-480-473B-4

  Query Match             62.1%;  Score 95;  DB 2;  Length 805;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        535 DLDLEMLAPYIPMDDDFQL 553


RESULT 13
US-08-915-213-4
; Sequence 4, Application US/08915213
; Patent No. 6020462
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/915,213
;      FILING DATE:  20-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  805 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-915-213-4

  Query Match             62.1%;  Score 95;  DB 3;  Length 805;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        535 DLDLEMLAPYIPMDDDFQL 553


RESULT 14
US-09-235-217-4
; Sequence 4, Application US/09235217
; Patent No. 6222018
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/235,217
```

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;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/480,473
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haile, Lisa A.
;       REGISTRATION NUMBER:  38,347
;       REFERENCE/DOCKET NUMBER:  07265/053001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/678-5070
;       TELEFAX:  619/678-5099
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  805 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-235-217-4

  Query Match             62.1%;  Score 95;  DB 3;  Length 805;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        535 DLDLEMLAPYIPMDDDFQL 553


RESULT 15
PCT-US96-10251-4
; Sequence 4, Application PC/TUS9610251
;  GENERAL INFORMATION:
;    APPLICANT:  The Johns Hopkins University School of Medicine
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10251
;      FILING DATE:  06-JUN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  805 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-10251-4

  Query Match             62.1%;  Score 95;  DB 5;  Length 805;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        535 DLDLEMLAPYIPMDDDFQL 553


RESULT 16
US-08-785-241-7
; Sequence 7, Application US/08785241
; Patent No. 5695963
;  GENERAL INFORMATION:
;    APPLICANT:  McKnight, Steven L.
;    APPLICANT:  Russell, David W.
;    APPLICANT:  Tian, Hui
;    TITLE OF INVENTION:  Endothelial PAS Domain Protein
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,241
;      FILING DATE:  17-JAN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UTSD:1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  810 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-785-241-7

  Query Match             62.1%;  Score 95;  DB 1;  Length 810;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        543 DLDLEMLAPYIPMDDDFQL 561


RESULT 17
US-09-438-833-12
; Sequence 12, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia & Upjohn
;  TITLE OF INVENTION: Protein variants
;  FILE REFERENCE: 1848
;  CURRENT APPLICATION NUMBER: US/09/438,833
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 813
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Description of Artificial Sequence: Subdomain
;   OTHER INFORMATION: 1-813 of human HIF-1 alpha
US-09-438-833-12

  Query Match             62.1%;  Score 95;  DB 4;  Length 813;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 18
US-08-785-241-6
; Sequence 6, Application US/08785241
; Patent No. 5695963
;  GENERAL INFORMATION:
;    APPLICANT:  McKnight, Steven L.
;    APPLICANT:  Russell, David W.
;    APPLICANT:  Tian, Hui
;    TITLE OF INVENTION:  Endothelial PAS Domain Protein
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,241
;      FILING DATE:  17-JAN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UTSD:1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  826 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-785-241-6

  Query Match             62.1%;  Score 95;  DB 1;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 19
US-08-480-473B-2
; Sequence 2, Application US/08480473B
; Patent No. 5882914
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,473B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  826 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-480-473B-2

  Query Match             62.1%;  Score 95;  DB 2;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 20
US-08-915-213-2
; Sequence 2, Application US/08915213
; Patent No. 6020462
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/915,213
;      FILING DATE:  20-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
```

```
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  826 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-915-213-2

  Query Match             62.1%;  Score 95;  DB 3;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 21
US-09-148-547-2
; Sequence 2, Application US/09148547
; Patent No. 6124131
; GENERAL INFORMATION:
;  APPLICANT: Semenza, Gregg L.
;  TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
;  FILE REFERENCE: 07265/151001
;  CURRENT APPLICATION NUMBER: US/09/148,547
;  CURRENT FILING DATE: 1998-08-25
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-148-547-2

  Query Match             62.1%;  Score 95;  DB 3;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 22
US-09-235-217-2
; Sequence 2, Application US/09235217
; Patent No. 6222018
;  GENERAL INFORMATION:
;    APPLICANT:  Semenza, Gregg L.
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/235,217
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/480,473
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  826 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-235-217-2

  Query Match             62.1%;  Score 95;  DB 3;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 23
US-09-380-662-23
; Sequence 23, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
;  APPLICANT: Caniggia, Isabella
;  APPLICANT:  Post, Martin
;  APPLICANT:  Lye, Stephen
;  TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
;  FILE REFERENCE: 11757.38USWO
;  CURRENT APPLICATION NUMBER: US/09/380,662
;  CURRENT FILING DATE:  1999-12-21
;  PRIOR APPLICATION NUMBER: PCT/CA98/00180
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: US 60/039,919
;  PRIOR FILING DATE: 1997-03-07
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-380-662-23

  Query Match             62.1%;  Score 95;  DB 3;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 24
US-09-438-833-1
; Sequence 1, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia & Upjohn
;  TITLE OF INVENTION: Protein variants
;  FILE REFERENCE: 1848
;  CURRENT APPLICATION NUMBER: US/09/438,833
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
```

; VOLUME: 92
; PAGES: 5510-5514
; DATABASE ACCESSION NUMBER: GenBank U22431
; DATABASE ENTRY DATE: 1995-06-28
US-09-438-833-1

  Query Match 62.1%; Score 95; DB 4; Length 826;
  Best Local Similarity 94.7%; Pred. No. 2e-05;
  Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
       ||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 25
US-09-702-705-330
; Sequence 330, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-330

  Query Match 62.1%; Score 95; DB 4; Length 826;
  Best Local Similarity 94.7%; Pred. No. 2e-05;
  Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
       ||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 26
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-330

  Query Match 62.1%; Score 95; DB 4; Length 826;
  Best Local Similarity 94.7%; Pred. No. 2e-05;
  Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
       ||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 27
US-09-383-581-2
; Sequence 2, Application US/09383581
; Patent No. 6562799
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/09/383,581
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-581-2

  Query Match 62.1%; Score 95; DB 4; Length 826;
  Best Local Similarity 94.7%; Pred. No. 2e-05;
  Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
       ||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 28
US-09-614-124B-330
; Sequence 330, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-330

  Query Match 62.1%; Score 95; DB 4; Length 826;
  Best Local Similarity 94.7%; Pred. No. 2e-05;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574
```

RESULT 29
US-09-671-325-330
; Sequence 330, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-330

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574
```

RESULT 30
US-09-589-184-330
; Sequence 330, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-330

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574
```

RESULT 31
US-09-658-824-330
; Sequence 330, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-330

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574
```

RESULT 32
US-09-959-873B-18
; Sequence 18, Application US/09959873B
; Patent No. 6787326
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/09/959,873B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-959-873B-18

Query Match 62.1%; Score 95; DB 4; Length 826;
Best Local Similarity 94.7%; Pred. No. 2e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
```

```
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 33
US-09-949-016-6089
; Sequence 6089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6089
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6089

  Query Match             62.1%;  Score 95;  DB 4;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 34
US-09-967-388-4
; Sequence 4, Application US/09967388
; Patent No. 6838430
; GENERAL INFORMATION:
;  APPLICANT: JEFFEREY M. ARBEIT
;  TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
;  TITLE OF INVENTION:  WOUND HEALING
;  FILE REFERENCE: UC077.001A
;  CURRENT APPLICATION NUMBER: US/09/967,388
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-967-388-4

  Query Match             62.1%;  Score 95;  DB 4;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 35
PCT-US96-10251-2
; Sequence 2, Application PC/TUS9610251
;  GENERAL INFORMATION:
;    APPLICANT:  The Johns Hopkins University School of Medicine
;    TITLE OF INVENTION:  HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10251
;      FILING DATE:  06-JUN-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/053WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  826 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-10251-2

  Query Match             62.1%;  Score 95;  DB 5;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 36
US-09-919-039-149
; Sequence 149, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 149
;   LENGTH: 827
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 1250434CD1
US-09-919-039-149

  Query Match             62.1%;  Score 95;  DB 4;  Length 827;
  Best Local Similarity   94.7%;  Pred. No. 2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        557 DLDLEMLAPYIPMDDDFQL 575


RESULT 37
US-09-972-784-5
```

```
; Sequence 5, Application US/09972784
; Patent No. 6566088
; GENERAL INFORMATION:
;  APPLICANT: McKnight, Steven L.
;  APPLICANT:  Bruik, Richard K.
;  TITLE OF INVENTION: Prolyl-4-Hydroxylases
;  FILE REFERENCE: UTSD0871
;  CURRENT APPLICATION NUMBER: US/09/972,784
;  CURRENT FILING DATE:  2001-10-04
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: sequence derived from HIF-a ODD domain.
US-09-972-784-5

  Query Match            54.2%;  Score 83;  DB 4;  Length 19;
  Best Local Similarity  84.2%;  Pred. No. 1.3e-05;
  Matches   16;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||| ||:||| ||||||
Db          1 DLDLEALAPYIPADDDFQL 19


RESULT 38
US-09-374-454-2
; Sequence 2, Application US/09374454
; Patent No. 6395548
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT: Maemura, Koji
;  APPLICANT: Hsieh, Chung-Ming
;  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
;  FILE REFERENCE: 05433/037001
;  CURRENT APPLICATION NUMBER: US/09/374,454
;  CURRENT FILING DATE: 1999-08-13
;  EARLIER APPLICATION NUMBER: US 60/096,515
;  EARLIER FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-374-454-2

  Query Match            46.1%;  Score 70.5;  DB 3;  Length 205;
  Best Local Similarity  75.0%;  Pred. No. 0.014;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db         38 ELDLETLAPYIPMDGEDFQL 57


RESULT 39
US-08-785-241-4
; Sequence 4, Application US/08785241
; Patent No. 5695963
;  GENERAL INFORMATION:
;    APPLICANT:  McKnight, Steven L.
;    APPLICANT:  Russell, David W.
;    APPLICANT:  Tian, Hui
;    TITLE OF INVENTION:  Endothelial PAS Domain Protein
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,241
;      FILING DATE:  17-JAN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UTSD:1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  870 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-785-241-4

  Query Match            46.1%;  Score 70.5;  DB 1;  Length 870;
  Best Local Similarity  75.0%;  Pred. No. 0.078;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 40
US-09-374-454-6
; Sequence 6, Application US/09374454
; Patent No. 6395548
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT: Maemura, Koji
;  APPLICANT: Hsieh, Chung-Ming
;  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
;  FILE REFERENCE: 05433/037001
;  CURRENT APPLICATION NUMBER: US/09/374,454
;  CURRENT FILING DATE: 1999-08-13
;  EARLIER APPLICATION NUMBER: US 60/096,515
;  EARLIER FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 870
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-374-454-6

  Query Match            46.1%;  Score 70.5;  DB 3;  Length 870;
  Best Local Similarity  75.0%;  Pred. No. 0.078;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 41
US-08-785-241-5
; Sequence 5, Application US/08785241
; Patent No. 5695963
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  McKnight, Steven L.
;    APPLICANT:  Russell, David W.
;    APPLICANT:  Tian, Hui
;    TITLE OF INVENTION:  Endothelial PAS Domain Protein
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,241
;      FILING DATE:  17-JAN-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UTSD:1229
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  875 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-785-241-5

  Query Match             46.1%;  Score 70.5;  DB 1;  Length 875;
  Best Local Similarity   75.0%;  Pred. No. 0.079;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 42
US-08-450-257-58
; Sequence 58, Application US/08450257
; Patent No. 5652122
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,257
;      FILING DATE:  25-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/235,403
;      FILING DATE:  28-APR-1994
;      APPLICATION NUMBER:  US 07/934,375
;      FILING DATE:  21-AUG-1992
;      APPLICATION NUMBER:  US 07/098,766
;      FILING DATE:  28-JUL-1993
;      APPLICATION NUMBER:  PCT/US93/07833
;      FILING DATE:  19-AUG-1993
;      APPLICATION NUMBER:  US 07/454,450
;      FILING DATE:  21-DEC-1989
;      APPLICATION NUMBER:  US 07/636,662
;      FILING DATE:  02-JAN-1991
;      APPLICATION NUMBER:  US 08/158,015
;      FILING DATE:  24-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B170 CIP 2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  385 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-450-257-58

  Query Match             45.1%;  Score 69;  DB 1;  Length 385;
  Best Local Similarity   62.5%;  Pred. No. 0.049;
  Matches   15;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPM 24
              |||||||||| |    | :  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 43
US-08-450-246-58
; Sequence 58, Application US/08450246
; Patent No. 5670617
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,246
;      FILING DATE:  25-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/235,403
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;       FILING DATE:  28-APR-1994
;       APPLICATION NUMBER:  US 07/934,375
;       FILING DATE:  21-AUG-1992
;       APPLICATION NUMBER:  US 07/098,766
;       FILING DATE:  28-JUL-1993
;       APPLICATION NUMBER:  PCT/US93/07833
;       FILING DATE:  19-AUG-1993
;       APPLICATION NUMBER:  US 07/454,450
;       FILING DATE:  21-DEC-1989
;       APPLICATION NUMBER:  US 07/636,662
;       FILING DATE:  02-JAN-1991
;       APPLICATION NUMBER:  US 08/158,015
;       FILING DATE:  24-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haley Jr., James F.
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  B170 CIP 2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;       TELEX:  14-8367
;   INFORMATION FOR SEQ ID NO:  58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  385 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-450-246-58

  Query Match             45.1%;  Score 69;  DB 1;  Length 385;
  Best Local Similarity   62.5%;  Pred. No. 0.049;
  Matches   15;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPM 24
              ||||||||||| |    | :  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 44
US-08-450-098-58
; Sequence 58, Application US/08450098
; Patent No. 5674980
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,098
;      FILING DATE:  25-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/235,403
;      FILING DATE:  28-APR-1994
;      APPLICATION NUMBER:  US 07/934,375
;      FILING DATE:  21-AUG-1992
;      APPLICATION NUMBER:  US 07/098,766
;      FILING DATE:  28-JUL-1993
;      APPLICATION NUMBER:  PCT/US93/07833
;      FILING DATE:  19-AUG-1993
;      APPLICATION NUMBER:  US 07/454,450
;      FILING DATE:  21-DEC-1989
;      APPLICATION NUMBER:  US 07/636,662
;      FILING DATE:  02-JAN-1991
;      APPLICATION NUMBER:  US 08/158,015
;      FILING DATE:  24-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B170 CIP 2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  385 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-450-098-58

  Query Match             45.1%;  Score 69;  DB 1;  Length 385;
  Best Local Similarity   62.5%;  Pred. No. 0.049;
  Matches   15;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPM 24
              ||||||||||| |    | :  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 45
US-08-451-233-58
; Sequence 58, Application US/08451233
; Patent No. 5747641
;  GENERAL INFORMATION:
;    APPLICANT:  FRANKEL, Alan
;    APPLICANT:  PABO, Carl
;    APPLICANT:  BARSOUM, James G.
;    APPLICANT:  FAWELL, Stephen E.
;    APPLICANT:  PEPINSKY, R. B.
;    TITLE OF INVENTION:  TAT-DERIVED TRANSPORT POLYPEPTIDES
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,233
;      FILING DATE:  25-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/235,403
;      FILING DATE:  28-APR-1994
;      APPLICATION NUMBER:  US 07/934,375
;      FILING DATE:  21-AUG-1992
;      APPLICATION NUMBER:  US 07/098,766
;      FILING DATE:  28-JUL-1993
;      APPLICATION NUMBER:  PCT/US93/07833
;      FILING DATE:  19-AUG-1993
;      APPLICATION NUMBER:  US 07/454,450
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; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-451-233-58

Query Match 45.1%; Score 69; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 0.049;
Matches 15; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAXYIPM 24
||||||||||| | | : ||
Db 2 YGRKKRRQRRRPLSQAQLMPSPPM 25

RESULT 46
US-08-450-236-58
; Sequence 58, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,236
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-236-58

Query Match 45.1%; Score 69; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 0.049;
Matches 15; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAXYIPM 24
||||||||||| | | : ||
Db 2 YGRKKRRQRRRPLSQAQLMPSPPM 25

RESULT 47
US-08-235-403-58
; Sequence 58, Application US/08235403
; Patent No. 6316003
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,403
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:

```
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  385 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-235-403-58

  Query Match             45.1%;  Score 69;  DB 3;  Length 385;
  Best Local Similarity   62.5%;  Pred. No. 0.049;
  Matches   15;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDDLEMLAXYIPM 24
              ||||||||||| |    | :  ||
Db          2 YGRKKRRQRRRPLSQAQLMPSPPM 25


RESULT 48
US-08-706-741B-87
; Sequence 87, Application US/08706741B
; Patent No. 5955593
;  GENERAL INFORMATION:
;    APPLICANT:  KORSMEYER, STANLEY J.
;    TITLE OF INVENTION:  BH3 INTERACTING DOMAIN DEATH AGONIST
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWELL & HAFERKAMP, L.C.
;      STREET:  7733 FORSYTH BLVD., SUITE 1400
;      CITY:  ST. LOUIS
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  63146
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/706,741B
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOLLAND, DONALD R.
;      REGISTRATION NUMBER:  35,197
;      REFERENCE/DOCKET NUMBER:  965017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 727-5188
;      TELEFAX:  (314) 727-6092
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-706-741B-87

  Query Match             41.2%;  Score 63;  DB 2;  Length 32;
  Best Local Similarity   48.1%;  Pred. No. 0.019;
  Matches   13;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDDLEMLAXYIPMDDD 27
              ||||||||||    :  :|:::    |
Db          1 YGRKKRRQRRRGEIIHNIARHLAQIGD 27


RESULT 49
US-08-924-695A-87
; Sequence 87, Application US/08924695A
; Patent No. 5998583
;  GENERAL INFORMATION:
;    APPLICANT:  KORSMEYER, STANLEY J.
;    TITLE OF INVENTION:  BH3 INTERACTING DOMAIN DEATH AGONIST
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOWELL & HAFERKAMP, L.C.
;      STREET:  7733 FORSYTH BLVD., SUITE 1400
;      CITY:  ST. LOUIS
;      STATE:  MISSOURI
;      COUNTRY:  USA
;      ZIP:  63105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/924,695A
;      FILING DATE:  09-SEP-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOLLAND, DONALD R.
;      REGISTRATION NUMBER:  35,197
;      REFERENCE/DOCKET NUMBER:  971798
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 727-5188
;      TELEFAX:  (314) 727-6092
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-924-695A-87

  Query Match             41.2%;  Score 63;  DB 2;  Length 32;
  Best Local Similarity   48.1%;  Pred. No. 0.019;
  Matches   13;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDDLEMLAXYIPMDDD 27
              ||||||||||    :  :|:::    |
Db          1 YGRKKRRQRRRGEIIHNIARHLAQIGD 27


RESULT 50
US-09-041-886-50
; Sequence 50, Application US/09041886
; Patent No. 6235872
;  GENERAL INFORMATION:
;    APPLICANT:  Bredesen, Dale E.
;    APPLICANT:  Rabizadeh, Sharroz
;    TITLE OF INVENTION:  Proapoptotic Peptides, Dependence
;    TITLE OF INVENTION:  Polypeptides and Methods of Use
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/041,886
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
```

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-50

Query Match 39.2%; Score 60; DB 3; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.045;
Matches 15; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

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Qy          2 GRKKRRQRRR----DLDLEMLAX 20
              ||||||||||    || |  ||:
Db          1 GRKKRRQRRRPPGGDLSLARLAT 23
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Search completed: February 8, 2005, 20:34:02
Job time : 43.6842 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 20:15:22 ; Search time 117.895 Seconds
(without alignments)
82.880 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 153
Sequence: 1 YGRKKRRQRRRDLDLEMLAXYIPMDDDFQL 30

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	95	62.1	19	16	US-10-901-583-8	Sequence 8, Appli
2	95	62.1	20	14	US-10-101-662A-15	Sequence 15, Appl
3	95	62.1	20	14	US-10-287-670-15	Sequence 15, Appl
4	95	62.1	20	14	US-10-287-670-25	Sequence 25, Appl
5	95	62.1	34	16	US-10-901-583-9	Sequence 9, Appli
6	95	62.1	54	9	US-09-922-958-5	Sequence 5, Appli
7	95	62.1	409	15	US-10-425-833-8	Sequence 8, Appli
8	95	62.1	466	15	US-10-425-833-9	Sequence 9, Appli
9	95	62.1	538	15	US-10-425-833-6	Sequence 6, Appli
10	95	62.1	542	15	US-10-264-049-2606	Sequence 2606, Ap
11	95	62.1	595	15	US-10-425-833-7	Sequence 7, Appli
12	95	62.1	632	15	US-10-425-833-10	Sequence 10, Appl
13	95	62.1	823	14	US-10-205-342-13	Sequence 13, Appl
14	95	62.1	826	9	US-09-922-958-4	Sequence 4, Appli
15	95	62.1	826	9	US-09-833-790-235	Sequence 235, App
16	95	62.1	826	9	US-09-736-457-330	Sequence 330, App
17	95	62.1	826	9	US-09-902-941-330	Sequence 330, App
18	95	62.1	826	9	US-09-849-626-330	Sequence 330, App
19	95	62.1	826	10	US-09-967-388-4	Sequence 4, Appli
20	95	62.1	826	10	US-09-476-300-330	Sequence 330, App
21	95	62.1	826	13	US-10-028-158-23	Sequence 23, Appl
22	95	62.1	826	13	US-10-101-812-10	Sequence 10, Appl
23	95	62.1	826	14	US-10-101-662A-9	Sequence 9, Appli
24	95	62.1	826	14	US-10-101-816-2	Sequence 2, Appli
25	95	62.1	826	14	US-10-017-754-330	Sequence 330, App
26	95	62.1	826	14	US-10-115-987B-14	Sequence 14, Appl
27	95	62.1	826	14	US-10-287-670-9	Sequence 9, Appli
28	95	62.1	826	14	US-10-113-872-330	Sequence 330, App
29	95	62.1	826	14	US-10-423-419-2	Sequence 2, Appli
30	95	62.1	826	15	US-10-283-017-330	Sequence 330, App
31	95	62.1	826	16	US-10-901-583-18	Sequence 18, Appl
32	95	62.1	827	10	US-09-919-039-149	Sequence 149, App
33	95	62.1	827	14	US-10-247-671-137	Sequence 137, App
34	90	58.8	826	14	US-10-101-816-5	Sequence 5, Appli
35	90	58.8	826	14	US-10-101-816-6	Sequence 6, Appli
36	90	58.8	826	14	US-10-101-816-7	Sequence 7, Appli
37	83	54.2	19	14	US-10-313-643A-5	Sequence 5, Appli
38	83	54.2	19	14	US-10-313-551A-5	Sequence 5, Appli
39	81	52.9	297	15	US-10-296-115-933	Sequence 933, App
40	81	52.9	705	14	US-10-154-386-2	Sequence 2, Appli
41	70.5	46.1	205	14	US-10-121-235-2	Sequence 2, Appli
42	70.5	46.1	870	14	US-10-121-235-6	Sequence 6, Appli
43	65	42.5	169	9	US-09-981-286A-7	Sequence 7, Appli
44	63.5	41.5	870	14	US-10-101-816-4	Sequence 4, Appli
45	61.5	40.2	23	13	US-10-024-935-11	Sequence 11, Appl
46	61.5	40.2	23	15	US-10-603-409-11	Sequence 11, Appl
47	61	39.9	22	9	US-09-949-196-8	Sequence 8, Appli
48	61	39.9	22	9	US-09-949-196-32	Sequence 32, Appl
49	61	39.9	23	14	US-10-311-111-34	Sequence 34, Appl
50	61	39.9	107	14	US-10-083-815-71	Sequence 71, Appl
51	60.5	39.5	23	13	US-10-024-935-10	Sequence 10, Appl
52	60.5	39.5	23	15	US-10-603-409-10	Sequence 10, Appl
53	59	38.6	254	16	US-10-437-963-196272	Sequence 196272,
54	58.5	38.2	17	10	US-09-847-946A-141	Sequence 141, App
55	58.5	38.2	17	10	US-09-847-946A-142	Sequence 142, App
56	58.5	38.2	20	13	US-10-024-935-8	Sequence 8, Appli
57	58.5	38.2	20	15	US-10-603-409-8	Sequence 8, Appli
58	58.5	38.2	195	9	US-09-949-780-6	Sequence 6, Appli
59	58	37.9	11	9	US-09-779-791A-1	Sequence 1, Appli
60	58	37.9	11	9	US-09-780-070-37	Sequence 37, Appl
61	58	37.9	11	9	US-09-815-108-9	Sequence 9, Appli
62	58	37.9	11	9	US-09-886-404-13	Sequence 13, Appl
63	58	37.9	11	9	US-09-805-805-8	Sequence 8, Appli
64	58	37.9	11	9	US-09-821-821-24	Sequence 24, Appl
65	58	37.9	11	9	US-09-895-943-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-901-583-8
; Sequence 8, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Motif
US-10-901-583-8

Query Match 62.1%; Score 95; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
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Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 2
US-10-101-662A-15
; Sequence 15, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-101-662A-15

Query Match 62.1%; Score 95; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
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Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 3
US-10-287-670-15
; Sequence 15, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009CIP1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Wherein Xaa is hydroxyproline
US-10-287-670-15

Query Match 62.1%; Score 95; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
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Db 1 DLDLEMLAXYIPMDDDFQL 19

RESULT 4
US-10-287-670-25
; Sequence 25, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009CIP1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816

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;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-670-25

  Query Match             62.1%;  Score 95;  DB 14;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 5
US-10-901-583-9
; Sequence 9, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
;  APPLICANT: Ratcliffe, Peter John
;  APPLICANT:  Maxwell, Patrick Henry
;  APPLICANT:  Pugh, Christopher William
;  TITLE OF INVENTION: Interaction Between the VHL Tumour
;  TITLE OF INVENTION:  Suppressor and Hypoxia Inducible Factor, and Assay Methods
;  TITLE OF INVENTION:  Relating Thereto
;  FILE REFERENCE: 3547.1000-000
;  CURRENT APPLICATION NUMBER: US/10/901,583
;  CURRENT FILING DATE:  2004-07-29
;  PRIOR APPLICATION NUMBER: US/09/959,873
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: PCT/GB00/01826
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: GB9911047.0
;  PRIOR FILING DATE: 1999-05-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-901-583-9

  Query Match             62.1%;  Score 95;  DB 16;  Length 34;
  Best Local Similarity   94.7%;  Pred. No. 3.4e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db          8 DLDLEMLAPYIPMDDDFQL 26


RESULT 6
US-09-922-958-5
; Sequence 5, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
;  APPLICANT: POELLINGER, Lorenz
;  APPLICANT:  PEREIRA, Teresa
;  APPLICANT:  RUAS, Jorge
;  TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
;  TITLE OF INVENTION:  THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
;  FILE REFERENCE: 3743/49008
;  CURRENT APPLICATION NUMBER: US/09/922,958
;  CURRENT FILING DATE:  2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/223,480
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-922-958-5

  Query Match             62.1%;  Score 95;  DB 9;  Length 54;
  Best Local Similarity   94.7%;  Pred. No. 5.7e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db         25 DLDLEMLAPYIPMDDDFQL 43


RESULT 7
US-10-425-833-8
; Sequence 8, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 409
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-8

  Query Match             62.1%;  Score 95;  DB 15;  Length 409;
  Best Local Similarity   94.7%;  Pred. No. 5.4e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 8
US-10-425-833-9
; Sequence 9, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
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;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

  Query Match             62.1%;  Score 95;  DB 15;  Length 466;
  Best Local Similarity   94.7%;  Pred. No. 6.3e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 9
US-10-425-833-6
; Sequence 6, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 538
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-6

  Query Match             62.1%;  Score 95;  DB 15;  Length 538;
  Best Local Similarity   94.7%;  Pred. No. 7.3e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        364 DLDLEMLAPYIPMDDDFQL 382


RESULT 10
US-10-264-049-2606
; Sequence 2606, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA133P1
;  CURRENT APPLICATION NUMBER: US/10/264,049
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/18569
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: US 60/209,467
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 4360
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2606
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-049-2606

  Query Match             62.1%;  Score 95;  DB 15;  Length 542;
  Best Local Similarity   94.7%;  Pred. No. 7.4e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        272 DLDLEMLAPYIPMDDDFQL 290


RESULT 11
US-10-425-833-7
; Sequence 7, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 595
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-7

  Query Match             62.1%;  Score 95;  DB 15;  Length 595;
  Best Local Similarity   94.7%;  Pred. No. 8.2e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        364 DLDLEMLAPYIPMDDDFQL 382


RESULT 12
US-10-425-833-10
; Sequence 10, Application US/10425833
; Publication No. US20040018606A1
; GENERAL INFORMATION:
;  APPLICANT: Bohl, Delphine
;  APPLICANT:  Heard, Jean Michael
;  TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1
;  TITLE OF INVENTION:  chimeric transactivator
;  FILE REFERENCE: 235748US0
;  CURRENT APPLICATION NUMBER: US/10/425,833
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: US 60/376,269
;  PRIOR FILING DATE: 2002-04-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 632
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-10

  Query Match             62.1%;  Score 95;  DB 15;  Length 632;
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  Best Local Similarity   94.7%;  Pred. No. 8.8e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 13
US-10-205-342-13
; Sequence 13, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
;  APPLICANT: Warner-Lambert Company
;  APPLICANT:  Lee, Kevin
;  APPLICANT:  Dixon, Alistair
;  APPLICANT:  Brooksbank, Robert
;  APPLICANT:  Pinnock, Robert
;  TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
;  FILE REFERENCE: WL-A-018198
;  CURRENT APPLICATION NUMBER: US/10/205,342
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: GB 0118354.0
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 823
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Protein: hypoxia-inducible factor-1 alpha
US-10-205-342-13

  Query Match             62.1%;  Score 95;  DB 14;  Length 823;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 14
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
;  APPLICANT: POELLINGER, Lorenz
;  APPLICANT:  PEREIRA, Teresa
;  APPLICANT:  RUAS, Jorge
;  TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE FACT
;  TITLE OF INVENTION:  THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
;  FILE REFERENCE: 3743/49008
;  CURRENT APPLICATION NUMBER: US/09/922,958
;  CURRENT FILING DATE:  2001-08-07
;  PRIOR APPLICATION NUMBER: US 60/223,480
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-922-958-4

  Query Match             62.1%;  Score 95;  DB 9;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 15
US-09-833-790-235
; Sequence 235, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
;  APPLICANT: Lodes, Michael J.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Mohamath, Raodoh
;  APPLICANT:  Indirias, Carol Y.
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.512
;  CURRENT APPLICATION NUMBER: US/09/833,790
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 440
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-833-790-235

  Query Match             62.1%;  Score 95;  DB 9;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 16
US-09-736-457-330
; Sequence 330, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-736-457-330

  Query Match             62.1%;  Score 95;  DB 9;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 17
```

```
US-09-902-941-330
; Sequence 330, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C17
;  CURRENT APPLICATION NUMBER: US/09/902,941
;  CURRENT FILING DATE:  2001-07-10
;  NUMBER OF SEQ ID NOS: 2002
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-941-330

  Query Match             62.1%;  Score 95;  DB 9;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 18
US-09-849-626-330
; Sequence 330, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
;  APPLICANT: Bangur, Chaitanya
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Switzer, Anne
;  APPLICANT:  McNeill, Patricia
;  APPLICANT:  Clapper, Jonathan
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C16
;  CURRENT APPLICATION NUMBER: US/09/849,626
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 1926
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-626-330

  Query Match             62.1%;  Score 95;  DB 9;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 19
US-09-967-388-4
; Sequence 4, Application US/09967388
; Publication No. US20030103956A1
; GENERAL INFORMATION:
;  APPLICANT: JEFFEREY M. ARBEIT
;  TITLE OF INVENTION: USE OF HIF-1ALPHA VARIANTS TO ACCELERATE
;  TITLE OF INVENTION:  WOUND HEALING
;  FILE REFERENCE: UC077.001A
;  CURRENT APPLICATION NUMBER: US/09/967,388
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-967-388-4

  Query Match             62.1%;  Score 95;  DB 10;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 20
US-09-476-300-330
; Sequence 330, Application US/09476300
; Publication No. US20030125245A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT: Bangur, Chaitanya S.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C3
;  CURRENT APPLICATION NUMBER: US/09/476,300
;  CURRENT FILING DATE: 1999-12-30
;  NUMBER OF SEQ ID NOS: 785
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 330
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-476-300-330

  Query Match             62.1%;  Score 95;  DB 10;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00012;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 21
US-10-028-158-23
; Sequence 23, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
;  APPLICANT: Caniggia, Isabella
;  APPLICANT:  Post, Martin
;  APPLICANT:  Lye, Stephen
;  TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
;  TITLE OF INVENTION:  TROPHOBLAST
;  FILE REFERENCE: 11757.38USWO
;  CURRENT APPLICATION NUMBER: US/10/028,158
;  CURRENT FILING DATE:  2001-12-20
;  PRIOR APPLICATION NUMBER: US/09/380,662
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: PCT/CA98/00180
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: US 60/039,919
```

; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-158-23

Query Match 62.1%; Score 95; DB 13; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 22
US-10-101-812-10
; Sequence 10, Application US/10101812
; Publication No. US20020192737A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Pharmaceuticals and Methods for Treating Hypoxia and
; TITLE OF INVENTION: Screening Methods Thereof
; FILE REFERENCE: 20363-014
; CURRENT APPLICATION NUMBER: US/10/101,812
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Target Peptide
US-10-101-812-10

Query Match 62.1%; Score 95; DB 13; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 23
US-10-101-662A-9
; Sequence 9, Application US/10101662A
; Publication No. US20030022198A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Livingston, David A
; APPLICANT: Kim, William
; TITLE OF INVENTION: Light Emitting Fusion Proteins and Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009
; CURRENT APPLICATION NUMBER: US/10/101,662A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-662A-9

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 24
US-10-101-816-2
; Sequence 2, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-2

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAAYIPMDDDFQL 574

RESULT 25
US-10-017-754-330
; Sequence 330, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-330

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 26
US-10-115-987B-14
; Sequence 14, Application US/10115987B
; Publication No. US20030148521A1
; GENERAL INFORMATION:
; APPLICANT: Bell, John C.; Stojdl, David F.;
; APPLICANT: Gray, Douglas A.; Sonenberg,
; APPLICANT: Nahum; Lichty, Brian
; TITLE OF INVENTION: Conditionally Replicative and
; TITLE OF INVENTION: Conditionally Active Viruses
; FILE REFERENCE: 42630-0001
; CURRENT APPLICATION NUMBER: US/10/115,987B
; CURRENT FILING DATE: 2002-03-03
; PRIOR APPLICATION NUMBER: US60/281,781
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: EditPad
; SEQ ID NO 14
; LENGTH: 826
; TYPE: PRT
; ORGANISM: homo Sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Wang et al.
; JOURNAL: Proceedings of the National Academy of Sciences
; VOLUME: 92
; PAGES: 5510-5514
; DATE: 1995
US-10-115-987B-14

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 27
US-10-287-670-9
; Sequence 9, Application US/10287670
; Publication No. US20030150005A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., et al.
; TITLE OF INVENTION: Transgenic Animals Expressing Light Emitting Fusion Proteins and
; TITLE OF INVENTION: Diagnostic and
; TITLE OF INVENTION: Therapeutic Methods Thereof
; FILE REFERENCE: 20363-009CIP1
; CURRENT APPLICATION NUMBER: US/10/287,670
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/101,662
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,812
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 10/101,816
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-670-9

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 28

US-10-113-872-330
; Sequence 330, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-330

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 29
US-10-423-419-2
; Sequence 2, Application US/10423419
; Publication No. US20030176349A1
; GENERAL INFORMATION:
; APPLICANT: Semenza, Gregg L.
; TITLE OF INVENTION: STABLE HYPOXIA INDUCIBLE FACTOR-1 alpha
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: JHU1500-1
; CURRENT APPLICATION NUMBER: US/10/423,419
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US/09/383,581
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/148,547
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-423-419-2

Query Match 62.1%; Score 95; DB 14; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 30
US-10-283-017-330
; Sequence 330, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-017-330

Query Match 62.1%; Score 95; DB 15; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 31
US-10-901-583-18
; Sequence 18, Application US/10901583
; Publication No. US20050003452A1
; GENERAL INFORMATION:
; APPLICANT: Ratcliffe, Peter John
; APPLICANT: Maxwell, Patrick Henry
; APPLICANT: Pugh, Christopher William
; TITLE OF INVENTION: Interaction Between the VHL Tumour
; TITLE OF INVENTION: Suppressor and Hypoxia Inducible Factor, and Assay Methods
; TITLE OF INVENTION: Relating Thereto
; FILE REFERENCE: 3547.1000-000
; CURRENT APPLICATION NUMBER: US/10/901,583
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/959,873
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/GB00/01826
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: GB9911047.0
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-583-18

Query Match 62.1%; Score 95; DB 16; Length 826;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 32
US-09-919-039-149
; Sequence 149, Application US/09919039
; Publication No. US20030108871A1

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1250434CD1
US-09-919-039-149

Query Match 62.1%; Score 95; DB 10; Length 827;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 33
US-10-247-671-137
; Sequence 137, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 137
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1250434CD1
US-10-247-671-137

Query Match 62.1%; Score 95; DB 14; Length 827;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 557 DLDLEMLAPYIPMDDDFQL 575

RESULT 34
US-10-101-816-5
; Sequence 5, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-5

Query Match 58.8%; Score 90; DB 14; Length 826;
Best Local Similarity 89.5%; Pred. No. 0.0006;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
|||||| |:||||||||||
Db 556 DLDLEMAAPYIPMDDDFQL 574

RESULT 35
US-10-101-816-6
; Sequence 6, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin Jr., William G
; APPLICANT: Ivan, Mircea
; TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: 20363-008
; CURRENT APPLICATION NUMBER: US/10/101,816
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/277,425
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,431
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,440
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/332,493
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,200
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/345,131
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/342,598
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/345,132
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/332,334
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 826

```
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-6

  Query Match             58.8%;  Score 90;  DB 14;  Length 826;
  Best Local Similarity   89.5%;  Pred. No. 0.0006;
  Matches   17;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||| |:||||||||||
Db        556 DLDLEMAAAYIPMDDDFQL 574


RESULT 36
US-10-101-816-7
; Sequence 7, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-7

  Query Match             58.8%;  Score 90;  DB 14;  Length 826;
  Best Local Similarity   89.5%;  Pred. No. 0.0006;
  Matches   17;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||| |:||||||||||
Db        556 DLDLEMAAAYIPMDDDFQL 574


RESULT 37
US-10-313-643A-5
; Sequence 5, Application US/10313643A
; Publication No. US20030153503A1
; GENERAL INFORMATION:
;  APPLICANT: Klaus, Stephen J.
;  APPLICANT:  Lin, Al Y.
;  APPLICANT:  Neff, Thomas B.
;  APPLICANT:  Wang, Qingjian
;  APPLICANT:  Arend, Michael P.
;  APPLICANT:  Flippin, Lee A.
;  APPLICANT:  Melekhov, Alexey G.
;  TITLE OF INVENTION: METHODS OF INCREASING ENDOGENOUS ERYTHROPOIETIN (EPO)
;  FILE REFERENCE: FP0601 US
;  CURRENT APPLICATION NUMBER: US/10/313,643A
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/349,659
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/386,488
;  PRIOR FILING DATE: 2002-06-05
;  PRIOR APPLICATION NUMBER: US 60/337,082
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: US 60/359,683
;  PRIOR FILING DATE: 2002-02-25
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
US-10-313-643A-5

  Query Match             54.2%;  Score 83;  DB 14;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 8.8e-05;
  Matches   16;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||| ||:||| ||||||
Db          1 DLDLEALAPYIPADDDFQL 19


RESULT 38
US-10-313-551A-5
; Sequence 5, Application US/10313551A
; Publication No. US20030176317A1
; GENERAL INFORMATION:
;  APPLICANT: Guenzler-Pukall, Volkmar
;  APPLICANT:  Neff, Thomas B.
;  APPLICANT:  Wang, Qingjian
;  APPLICANT:  Arend, Michael
;  APPLICANT:  Flippin, Lee A.
;  APPLICANT:  Melekhov, Alexey G.
;  TITLE OF INVENTION: STABILIZATION OF HYPOXIA INDUCIBLE FACTOR (HIF) ALPHA
;  FILE REFERENCE: FP0600 US
;  CURRENT APPLICATION NUMBER: US/10/313,551A
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/337,082
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: US 60/359,683
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: US 60/349,659
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: US 60/386,488
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
US-10-313-551A-5

  Query Match             54.2%;  Score 83;  DB 14;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 8.8e-05;
  Matches   16;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||| ||:||| ||||||
```

```
Db          1 DLDLEALAPYIPADDDFQL 19


RESULT 39
US-10-296-115-933
; Sequence 933, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq Inc
;  TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 784PCT
;  CURRENT APPLICATION NUMBER: US/10/296,115
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 933
;   LENGTH: 297
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-296-115-933

  Query Match             52.9%;  Score 81;  DB 15;  Length 297;
  Best Local Similarity   88.9%;  Pred. No. 0.0035;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        166 LDLEMLAPYISMDDDFQL 183


RESULT 40
US-10-154-386-2
; Sequence 2, Application US/10154386
; Publication No. US20030026793A1
; GENERAL INFORMATION:
;  APPLICANT: Angiogene Inc.
;  APPLICANT:  Guy, Louis-Georges
;  TITLE OF INVENTION: HIPOXIA INDUCING FACTORS AND USES THEREOF FOR INDUCING ANGIOGENES
;  TITLE OF INVENTION:  IMPROVING MUSCULAR FUNCTIONS
;  FILE REFERENCE: 5600-81
;  CURRENT APPLICATION NUMBER: US/10/154,386
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: US 60/292,630
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/354529
;  PRIOR FILING DATE: 2002-02-08
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-154-386-2

  Query Match             52.9%;  Score 81;  DB 14;  Length 705;
  Best Local Similarity   88.9%;  Pred. No. 0.0092;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        521 LDLEMLAPYISMDDDFQL 538


RESULT 41
US-10-121-235-2
; Sequence 2, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT:  Maemura, Koji
;  APPLICANT:  Hsieh, Chung-Ming
;  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
;  FILE REFERENCE: 05433/037001
;  CURRENT APPLICATION NUMBER: US/10/121,235
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/374,454
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: US 60/096,515
;  PRIOR FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-121-235-2

  Query Match             46.1%;  Score 70.5;  DB 14;  Length 205;
  Best Local Similarity   75.0%;  Pred. No. 0.07;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db         38 ELDLETLAPYIPMDGEDFQL 57


RESULT 42
US-10-121-235-6
; Sequence 6, Application US/10121235
; Publication No. US20030032609A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Mu-En
;  APPLICANT:  Maemura, Koji
;  APPLICANT:  Hsieh, Chung-Ming
;  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
;  FILE REFERENCE: 05433/037001
;  CURRENT APPLICATION NUMBER: US/10/121,235
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: US 09/374,454
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: US 60/096,515
;  PRIOR FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 870
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-121-235-6

  Query Match             46.1%;  Score 70.5;  DB 14;  Length 870;
  Best Local Similarity   75.0%;  Pred. No. 0.35;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 43
US-09-981-286A-7
; Sequence 7, Application US/09981286A
; Publication No. US20020192799A1
; GENERAL INFORMATION:
;  APPLICANT: Watowich, Stanley J.
;  APPLICANT:  Weaver, Scott C.
;  APPLICANT:  Davey, Robert A.
;  TITLE OF INVENTION: Drug Discovery Methods
;  FILE REFERENCE: 265.00260101
;  CURRENT APPLICATION NUMBER: US/09/981,286A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: US 60/240,187
;  PRIOR FILING DATE: 2000-10-13
```

```
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of tat-CCD
US-09-981-286A-7

  Query Match             42.5%;  Score 65;  DB 9;  Length 169;
  Best Local Similarity   81.2%;  Pred. No. 0.34;
  Matches   13;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLE 16
              |||||||||||  : ||
Db          2 YGRKKRRQRRRVMKLE 17


RESULT 44
US-10-101-816-4
; Sequence 4, Application US/10101816
; Publication No. US20030045686A1
; GENERAL INFORMATION:
;  APPLICANT: Kaelin Jr., William G
;  APPLICANT:  Ivan, Mircea
;  TITLE OF INVENTION: Muteins of Hypoxia Inducible Factor Alpha and Methods
;  TITLE OF INVENTION:  of Use Thereof
;  FILE REFERENCE: 20363-008
;  CURRENT APPLICATION NUMBER: US/10/101,816
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/277,425
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,431
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/277,440
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: 60/332,493
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,200
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/345,131
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/342,598
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/345,132
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/332,334
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 870
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIF Mutein
US-10-101-816-4

  Query Match             41.5%;  Score 63.5;  DB 14;  Length 870;
  Best Local Similarity   70.0%;  Pred. No. 3.4;
  Matches   14;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| : |||
Db        523 ELDLETLAAYIPMDGEGFQL 542


RESULT 45
US-10-024-935-11
; Sequence 11, Application US/10024935
; Publication No. US20020142966A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth Walter Bair
;  APPLICANT:  YingNan Pan Chen
;  APPLICANT:  Timothy Michael Ramsey
;  APPLICANT:  Michael Lloyd Sabio
;  APPLICANT:  Sushill  Kumar Sharma
;  TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
;  TITLE OF INVENTION:  Interaction for Cancer Therapy
;  FILE REFERENCE: 4-31664P1/Prov
;  CURRENT APPLICATION NUMBER: US/10/024,935
;  CURRENT FILING DATE:  2001-12-19
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-024-935-11

  Query Match             40.2%;  Score 61.5;  DB 13;  Length 23;
  Best Local Similarity   66.7%;  Pred. No. 0.11;
  Matches   14;  Conservative    3;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAX 20
              |||||||||||  : | : ||:
Db          1 YGRKKRRQRRRGETDHQYLAE 21


RESULT 46
US-10-603-409-11
; Sequence 11, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth Walter Bair
;  APPLICANT:  YingNan Pan Chen
;  APPLICANT:  Timothy Michael Ramsey
;  APPLICANT:  Michael Lloyd Sabio
;  APPLICANT:  Sushill  Kumar Sharma
;  TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
;  TITLE OF INVENTION:  Interaction for Cancer Therapy
;  FILE REFERENCE: 4-33243/P1/N1
;  CURRENT APPLICATION NUMBER: US/10/603,409
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: 10/024,935
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: PCT/EP1 /15006
;  PRIOR FILING DATE: 2001-12-19
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-11

  Query Match             40.2%;  Score 61.5;  DB 15;  Length 23;
  Best Local Similarity   66.7%;  Pred. No. 0.11;
  Matches   14;  Conservative    3;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAX 20
              |||||||||||  : | : ||:
Db          1 YGRKKRRQRRRGETDHQYLAE 21


RESULT 47
US-09-949-196-8
; Sequence 8, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
;  APPLICANT: Zealand Pharmaceuticals A/S
```

```
;  TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE
;  TITLE OF INVENTION:  TO DNA DAMAGE
;  FILE REFERENCE: 55888 (45487)
;  CURRENT APPLICATION NUMBER: US/09/949,196
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (22)..(22)
;   OTHER INFORMATION: NH2
US-09-949-196-8

  Query Match             39.9%;  Score 61;  DB 9;  Length 22;
  Best Local Similarity   65.0%;  Pred. No. 0.13;
  Matches   13;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAX 20
              ||||||||||  |   | :
Db          1 YGRKKRRQRRRLFDSPALCS 20


RESULT 48
US-09-949-196-32
; Sequence 32, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
;  APPLICANT: Zealand Pharmaceuticals A/S
;  TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE
;  TITLE OF INVENTION:  TO DNA DAMAGE
;  FILE REFERENCE: 55888 (45487)
;  CURRENT APPLICATION NUMBER: US/09/949,196
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (22)..(22)
;   OTHER INFORMATION: NH2
US-09-949-196-32

  Query Match             39.9%;  Score 61;  DB 9;  Length 22;
  Best Local Similarity   65.0%;  Pred. No. 0.13;
  Matches   13;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAX 20
              ||||||||||  |   | :
Db          1 YGRKKRRQRRRLFDSPSLCS 20


RESULT 49
US-10-311-111-34
; Sequence 34, Application US/10311111
; Publication No. US20030121065A1
; GENERAL INFORMATION:
;  APPLICANT: SHIBA, KIYOTAKA
;  TITLE OF INVENTION: MULTIFUNCTIONAL BASE SEQUENCE AND ARTIFICIAL GENE CONTAINING THE
;  FILE REFERENCE: 4439-4004
;  CURRENT APPLICATION NUMBER: US/10/311,111
;  CURRENT FILING DATE:  2002-12-13
;  PRIOR APPLICATION NUMBER: JP 2000-180997
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: Designed peptide
US-10-311-111-34

  Query Match             39.9%;  Score 61;  DB 14;  Length 23;
  Best Local Similarity   60.0%;  Pred. No. 0.13;
  Matches   12;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAX 20
              ||||||||||  ::   |:
Db          1 YGRKKRRQRRRAAEIRRQAQ 20


RESULT 50
US-10-083-815-71
; Sequence 71, Application US/10083815
; Publication No. US20030026781A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Christen M.
;  APPLICANT:  Clevenger, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
;  TITLE OF INVENTION:  ENDOGENOUS INHIBITOR OF ATP SYNTHASE, INCLUDING
;  TITLE OF INVENTION:  TREATMENT FOR DIABETES
;  FILE REFERENCE: 660088.435C2
;  CURRENT APPLICATION NUMBER: US/10/083,815
;  CURRENT FILING DATE:  2002-02-27
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-10-083-815-71

  Query Match             39.9%;  Score 61;  DB 14;  Length 107;
  Best Local Similarity   65.0%;  Pred. No. 0.74;
  Matches   13;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRDLDLEMLAX 20
              ||||||||||  :    ||:
Db         37 YGRKKRRQRRRGMAGSALAV 56


Search completed: February  8, 2005, 20:38:03
Job time : 118.895 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 19:40:51 ; Search time 160.526 Seconds
(without alignments)
72.280 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 153
Sequence: 1 YGRKKRRQRRRDLDLEMLAXYIPMDDDFQL 30

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	153	100.0	30	6	ABR82380	Abr82380 Hypoxia-i
2	138	90.2	1125	6	ABP57672	Abp57672 HIF-1 alp
3	138	90.2	1160	6	ABP57674	Abp57674 HIF-1 alp
4	136.5	89.2	1087	6	ABP57673	Abp57673 HIF-1 alp
5	136.5	89.2	1122	6	ABP57675	Abp57675 HIF-1 alp
6	118	77.1	28	7	AAO23532	Aao23532 Fluoresce
7	95	62.1	19	4	AAB49912	Aab49912 Human/mur
8	95	62.1	19	6	AAE30166	Aae30166 Peptide #
9	95	62.1	19	6	AAE30167	Aae30167 Peptide #
10	95	62.1	19	6	AAE30144	Aae30144 HIFalpha
11	95	62.1	19	6	AAE30162	Aae30162 Peptide #
12	95	62.1	19	6	AAE30172	Aae30172 Human HIF
13	95	62.1	19	6	AAE30158	Aae30158 HIF-1alph
14	95	62.1	19	6	ABR82378	Abr82378 Hypoxia-i
15	95	62.1	19	8	ADP56728	Adp56728 Substrate
16	95	62.1	19	8	ADP79479	Adp79479 Hypoxia i
17	95	62.1	20	6	ABP55440	Abp55440 Hypoxia-i
18	95	62.1	20	8	ADO22337	Ado22337 HIF-1alph
19	95	62.1	29	7	AAO23501	Aao23501 Murine HI
20	95	62.1	29	7	AAO23481	Aao23481 Murine HI
21	95	62.1	29	7	AAO23472	Aao23472 Murine HI
22	95	62.1	29	7	AAO23499	Aao23499 Murine HI
23	95	62.1	34	4	AAB49913	Aab49913 Human/mur
24	95	62.1	34	6	AAE30161	Aae30161 Peptide #
25	95	62.1	34	6	AAE30151	Aae30151 HIFalpha
26	95	62.1	54	3	AAY94637	Aay94637 HIF-1alph
27	95	62.1	54	7	AAO23490	Aao23490 Murine HI
28	95	62.1	54	7	AAO23530	Aao23530 Murine HI
29	95	62.1	54	7	AAO23528	Aao23528 Murine HI
30	95	62.1	54	7	AAO23519	Aao23519 Murine HI
31	95	62.1	54	7	AAO23529	Aao23529 Murine HI
32	95	62.1	54	7	AAO23493	Aao23493 Murine HI
33	95	62.1	116	3	AAY94632	Aay94632 HIF-1alph
34	95	62.1	288	3	AAY94633	Aay94633 HIF-1alph
35	95	62.1	301	3	AAY94634	Aay94634 HIF-1alph
36	95	62.1	311	3	AAY94631	Aay94631 HIF-1alph
37	95	62.1	409	8	ADO39389	Ado39389 Chimeric
38	95	62.1	444	4	AAB68415	Aab68415 Amino aci
39	95	62.1	466	8	ADO39390	Ado39390 Chimeric
40	95	62.1	538	8	ADO39387	Ado39387 Chimeric
41	95	62.1	542	5	ABP41474	Abp41474 Human ova
42	95	62.1	595	8	ADO39388	Ado39388 Chimeric
43	95	62.1	613	3	AAY94630	Aay94630 HIF-1alph
44	95	62.1	613	5	AAU77614	Aau77614 Human hyp
45	95	62.1	632	8	ADO39391	Ado39391 Chimeric
46	95	62.1	652	3	AAY94629	Aay94629 HIF-1alph
47	95	62.1	669	3	AAY84167	Aay84167 A variant
48	95	62.1	697	3	AAY84166	Aay84166 A variant
49	95	62.1	701	3	AAY84173	Aay84173 A variant
50	95	62.1	710	3	AAY84172	Aay84172 A variant
51	95	62.1	724	3	AAY84171	Aay84171 A variant
52	95	62.1	735	6	ABR82375	Abr82375 Hypoxia-i
53	95	62.1	735	8	ADN75066	Adn75066 Human hyp
54	95	62.1	749	3	AAY84170	Aay84170 A variant
55	95	62.1	756	3	AAY94635	Aay94635 HIF-1alph
56	95	62.1	789	3	AAY84169	Aay84169 A variant
57	95	62.1	789	6	ADA18535	Ada18535 Human hyp
58	95	62.1	789	6	ADA18533	Ada18533 Human hyp
59	95	62.1	789	6	ADA18534	Ada18534 Human hyp
60	95	62.1	805	2	AAW06558	Aaw06558 Hypoxia i
61	95	62.1	810	5	ABB57270	Abb57270 Mouse isc
62	95	62.1	813	3	AAY94636	Aay94636 HIF-1alph
63	95	62.1	823	6	ABR41951	Abr41951 Rat hypox
64	95	62.1	825	7	ADD44855	Add44855 Rat Prote
65	95	62.1	826	2	AAW06557	Aaw06557 Human hyp

ALIGNMENTS

RESULT 1
ABR82380
ID ABR82380 standard; peptide; 30 AA.
XX
AC ABR82380;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hypoxia-inducible factor 1 (HIF-1) alpha inhibitor ODD peptide.
XX
KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquillizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /label= Hyp
FT /note= "hydroxyproline"
XX
PN WO2003057820-A2.
XX
PD 17-JUL-2003.
XX
PF 04-OCT-2002; 2002WO-US031699.
XX
PR 21-DEC-2001; 2001US-00032361.

XX
PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
XX
PI Mcgrath K;
XX
DR WPI; 2003-645988/61.
XX
PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX
PS Claim 2; Page 9; 37pp; English.
XX
CC The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC an ODD peptide, a specific example of HIF-1 alpha peptide inhibitor,
CC containing the oxygen-dependent degradation sequence of HIF-1 alpha
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 153; DB 6; Length 30;
Best Local Similarity 96.7%; Pred. No. 5e-14;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRDLDLEMLAXYIPMDDDFQL 30
||||||||||||||||||||:||||||||||
Db 1 YGRKKRRQRRRDLDLEMLAPYIPMDDDFQL 30

RESULT 2
ABP57672
ID ABP57672 standard; protein; 1125 AA.
XX
AC ABP57672;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pCH/TAT/3-0 SEQ ID NO:39.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76624.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX
PS Example 3; Page 75-78; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1125 AA;

Query Match 90.2%; Score 138; DB 6; Length 1125;
Best Local Similarity 72.5%; Pred. No. 3.2e-10;
Matches 29; Conservative 1; Mismatches 0; Indels 10; Gaps 1;

Qy 1 YGRKKRRQRRR----------DLDLEMLAXYIPMDDDFQL 30
||||||||||| ||||||||:||||||||||
Db 11 YGRKKRRQRRRRSNPFSTQDTDLDLEMLAPYIPMDDDFQL 50

RESULT 3
ABP57674
ID ABP57674 standard; protein; 1160 AA.
XX
AC ABP57674;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pBAD/3-0 SEQ ID NO:43.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76626.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer

PT and improvement of microbial fermentation.
XX
PS Example 3; Page 95-99; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1160 AA;

Query Match 90.2%; Score 138; DB 6; Length 1160;
Best Local Similarity 72.5%; Pred. No. 3.3e-10;
Matches 29; Conservative 1; Mismatches 0; Indels 10; Gaps 1;

```
Qy          1 YGRKKRRQRRR----------DLDLEMLAXYIPMDDDFQL 30
              ||||||||||          ||||||||:||||||||||
Db         46 YGRKKRRQRRRRSNPFSTQDTDLDLEMLAPYIPMDDDFQL 85
```

RESULT 4
ABP57673
ID ABP57673 standard; protein; 1087 AA.
XX
AC ABP57673;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pCH/TAT/557-574 SEQ ID NO:41.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76625.
XX
PT New DNA encoding a polypeptide imparting relative stability under hypoxic
PT conditions to proteins within the cell, useful for treatment of cancer
PT and improvement of microbial fermentation.
XX
PS Example 3; Page 85-88; 144pp; Japanese.
XX
CC The present invention describes DNA encoding a hypoxia-inducible factor 1
CC alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC see ABP57669) (I), or encoding a fusion protein containing at least 16
CC residues of (I), a nuclear localisation signal (NLS), and another
CC protein, and imparting relative stability under specific conditions of
CC oxygen concentration within the cell. Also described: (1) vectors
CC containing the DNA; (2) cells transformed by the vectors; (3) producing
CC the fusion protein by culture of the transformed cells; (4) detecting
CC hypoxic conditions in cells by monitoring the stability of the protein
CC fused to (I) in cells transformed by vectors containing the DNA; (5)
CC regulating the stability of proteins within the cell by transformation
CC with the DNA; (6) inhibiting the development of cells under hypoxic
CC conditions, using the fusion protein; (7) fusion proteins encoded by the
CC DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC tension. (I) has cytostatic activity, and can be used for the
CC stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC solid tumour, and in gene therapy. (I) can be used in industrial
CC microbial fermentation, and in medicine, especially in the treatment of
CC tumours containing hypoxic regions. The present sequence represents a
CC fusion protein from the present invention
XX
SQ Sequence 1087 AA;

Query Match 89.2%; Score 136.5; DB 6; Length 1087;
Best Local Similarity 90.3%; Pred. No. 5e-10;
Matches 28; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 YGRKKRRQ-RRRDLDLEMLAXYIPMDDDFQL 30
              |||||||| ||| |||||||:||||||||||
Db         11 YGRKKRRQRRRRSLDLEMLAPYIPMDDDFQL 41
```

RESULT 5
ABP57675
ID ABP57675 standard; protein; 1122 AA.
XX
AC ABP57675;
XX
DT 30-APR-2003 (first entry)
XX
DE HIF-1 alpha related fusion protein pBAD/557-574 SEQ ID NO:45.
XX
KW Hypoxia-inducible factor 1 alpha; HIF-1 alpha; stabilisation; cytotoxic;
KW hypoxic; solid tumour; gene therapy; microbial fermentation; medicine;
KW tumour; nuclear localisation signal; oxygen dependent degradation domain;
KW NLS; ODD; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200299104-A1.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-JP005482.
XX
PR 05-JUN-2001; 2001JP-00169948.
PR 05-JUN-2001; 2001JP-00169949.
XX
PA (POKK) POLA CHEM IND INC.
PA (HIRA/) HIRAOKA M.
PA (KOND/) KONDOH S.
XX
PI Hiraoka M, Kondoh S, Harada H;
XX
DR WPI; 2003-148670/14.
DR N-PSDB; ABZ76627.
XX

```
PT   New DNA encoding a polypeptide imparting relative stability under hypoxic
PT   conditions to proteins within the cell, useful for treatment of cancer
PT   and improvement of microbial fermentation.
XX
PS   Example 3; Page 106-109; 144pp; Japanese.
XX
CC   The present invention describes DNA encoding a hypoxia-inducible factor 1
CC   alpha (HIF-1 alpha) amino acids 557 to 574 peptide (LDLEMLAPYIPMDDDFQL
CC   see ABP57669) (I), or encoding a fusion protein containing at least 16
CC   residues of (I), a nuclear localisation signal (NLS), and another
CC   protein, and imparting relative stability under specific conditions of
CC   oxygen concentration within the cell. Also described: (1) vectors
CC   containing the DNA; (2) cells transformed by the vectors; (3) producing
CC   the fusion protein by culture of the transformed cells; (4) detecting
CC   hypoxic conditions in cells by monitoring the stability of the protein
CC   fused to (I) in cells transformed by vectors containing the DNA; (5)
CC   regulating the stability of proteins within the cell by transformation
CC   with the DNA; (6) inhibiting the development of cells under hypoxic
CC   conditions, using the fusion protein; (7) fusion proteins encoded by the
CC   DNA; and (8) stabilisation of cells under specific conditions of oxygen
CC   tension. (I) has cytostatic activity, and can be used for the
CC   stabilisation of a cytotoxic protein within cells in hypoxic regions of a
CC   solid tumour, and in gene therapy. (I) can be used in industrial
CC   microbial fermentation, and in medicine, especially in the treatment of
CC   tumours containing hypoxic regions. The present sequence represents a
CC   fusion protein from the present invention
XX
SQ   Sequence 1122 AA;

  Query Match             89.2%;  Score 136.5;  DB 6;  Length 1122;
  Best Local Similarity   90.3%;  Pred. No. 5.1e-10;
  Matches   28;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQ-RRRDLDLEMLAXYIPMDDDFQL 30
              |||||||| ||| ||||||:||||||||||
Db         46 YGRKKRRQRRRRSLDLEMLAPYIPMDDDFQL 76


RESULT 6
AAO23532
ID   AAO23532 standard; peptide; 28 AA.
XX
AC   AAO23532;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Fluorescein HIV-TAT cellular uptake signal-HIF-1alpha peptide 2.
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; HIV; tat;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1. .13
FT                    /note= "HIV-TAT cellular uptake signal peptide"
FT   Modified-site    1
FT                    /note= "5'- fluorescein label"
FT   Peptide          14. .28
FT                    /note= "HIF-1alpha mutant peptide"
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Example 16; Fig 32; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. The present sequence represents a HIF-1alpha
CC   mutant peptide linked to a fluorescein labeled HIV-TAT cellular uptake
CC   signal peptide
XX
SQ   Sequence 28 AA;

  Query Match             77.1%;  Score 118;  DB 7;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 3.4e-09;
  Matches   25;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPMDDDFQL 30
              |||||||||||     ||||:||||||||||
Db          1 YGRKKRRQRRR--PPEMLAPYIPMDDDFQL 28


RESULT 7
AAB49912
ID   AAB49912 standard; peptide; 19 AA.
XX
AC   AAB49912;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Human/murine HIF-1alpha subunit conserved motif #8.
XX
KW   Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
KW   hypoxia inducible factor-1; cancer; ischaemia.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO200069908-A1.
XX
PD   23-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-GB001826.
XX
PR   12-MAY-1999;   99GB-00011047.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Ratcliffe PJ,  Maxwell PH,  Pugh CW;
XX
DR   WPI; 2001-025006/03.
XX
PT   Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
PT   subunit interaction modulators for treating ischemia by contacting a VHL
PT   protein and an HIF subunit protein with a putative modulator.
```

XX
PS Claim 13; Page 49; 56pp; English.
XX
CC The present invention describes a novel assay for use in identifying
CC modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
CC factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
CC contacting the VHL protein, the HIF-1alpha subunit and the putative
CC modulator under conditions where the former two would normally complex.
CC Modulators of this type are useful in the treatment of cancer and
CC ischaemic conditions such as coronary, cerebral and vascular
CC insufficiency
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 8
AAE30166
ID AAE30166 standard; peptide; 19 AA.
XX
AC AAE30166;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #6 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS Unidentified.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 247; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAGYIPMDDDFQL 19

RESULT 9
AAE30167
ID AAE30167 standard; peptide; 19 AA.
XX
AC AAE30167;
XX
DT 24-FEB-2003 (first entry)
XX
DE Peptide #7 used to block HIF-1alpha/pVHL interaction.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS Unidentified.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 247; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC interaction. This sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||

```
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 10
AAE30144
ID   AAE30144 standard; peptide; 19 AA.
XX
AC   AAE30144;
XX
DT   24-FEB-2003  (first entry)
XX
DE   HIFalpha subunit antagonist #1.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW   antagonist.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   2
FT                   /label= Hyp
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Claim 49; Page 196; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is HIFalpha subunit antagonist. This
CC   sequence is used in the invention
XX
SQ   Sequence 19 AA;

  Query Match             62.1%;  Score 95;  DB 6;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 3.6e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:|||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 11
AAE30162
ID   AAE30162 standard; peptide; 19 AA.
XX
AC   AAE30162;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Peptide #2 used to block HIF-1alpha/pVHL interaction.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Example 1; Page 246; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC   interaction. This sequence is used in the invention
XX
SQ   Sequence 19 AA;

  Query Match             62.1%;  Score 95;  DB 6;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 3.6e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:|||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 12
AAE30172
ID   AAE30172 standard; peptide; 19 AA.
XX
AC   AAE30172;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human HIF1-alpha peptide #2.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy;
```

KW human; HIF1-alpha.
XX
OS Homo sapiens.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Disclosure; Page 252; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is human HIF1-alpha peptide. This sequence
CC is used in the invention
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 13
AAE30158
ID AAE30158 standard; peptide; 19 AA.
XX
AC AAE30158;
XX
DT 24-FEB-2003 (first entry)
XX
DE HIF-1alpha pVHL minimal binding domain.
XX
KW Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW human.
XX
OS Homo sapiens.
XX
PN WO200274981-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-GB001381.
XX
PR 21-MAR-2001; 2001GB-00007123.
PR 02-AUG-2001; 2001GB-00018952.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Example 1; Page 245; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is HIF-1alpha pVHL minimal binding domain.
CC This sequence is used in the invention
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 14
ABR82378
ID ABR82378 standard; peptide; 19 AA.
XX
AC ABR82378;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hypoxia-inducible factor 1 (HIF-1) alpha peptide inhibitor.
XX
KW HIF-1; hypoxia-inducible factor 1; HIF-1 alpha; ubiquitination; EPO;
KW erythropoietin; vascular endothelial growth factor; VEGF; glycolytic;
KW tranquillizer; vulnerary; cardiant; cerebroprotective; angiogenesis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /label= Hyp
FT /note= "hydroxyproline"
XX
PN WO2003057820-A2.
XX
PD 17-JUL-2003.
XX
PF 04-OCT-2002; 2002WO-US031699.
XX
PR 21-DEC-2001; 2001US-00032361.
XX
PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX
PI Mcgrath K;
XX
DR WPI; 2003-645988/61.
XX
PT Novel peptide inhibitor of hypoxia-inducible factor 1 alpha
PT ubiquitination, and activator of vascular endothelial growth factor
PT transcription useful for treating tissue injuries including wounds,
PT surgical incisions.
XX
PS Claim 2; Page 8; 37pp; English.
XX
CC The invention relates to peptide inhibitors of hypoxia-inducible factor
CC (HIF-1) alpha ubiquitination. The peptide inhibitors thereby activate the
CC transcription of erythropoietin (EPO), vascular endothelial growth factor
CC (VEGF) and certain glycolytic enzymes. The peptide inhibitors are useful
CC for treating tissue injuries including wounds, surgical incisions,
CC chronic wounds, heart disease and stroke. The present sequence represents
CC a specific example of HIF-1 alpha peptide inhibitor, containing the
CC oxygen-dependent degradation sequence of HIF-1 alpha
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 15
ADP56728
ID ADP56728 standard; peptide; 19 AA.
XX
AC ADP56728;
XX
DT 09-SEP-2004 (first entry)
XX
DE Substrate peptide used in human HIF prolyl hydroxylase screening assay.
XX
KW fat metabolism; HIFalpha; hypoxia inducible factor alpha subunit;
KW atherosclerosis; diabetes; obesity; HIF prolyl hydroxylase substrate;
KW human; HIF-PH.
XX
OS Homo sapiens.
XX
PN WO2004052285-A2.
XX
PD 24-JUN-2004.
XX
PF 05-DEC-2003; 2003WO-US038690.
XX
PR 06-DEC-2002; 2002US-0431351P.
PR 06-JUN-2003; 2003US-0476331P.
PR 06-JUN-2003; 2003US-0476726P.
PR 04-DEC-2003; 2003US-00729167.
XX
PA (FIBR-) FIBROGEN INC.
XX
PI Fourney PD, Guenzler-Pukall V, Klaus SJ, Lin AY, Neff TB;
PI Seeley TW;
XX
DR WPI; 2004-468689/44.
XX
PT Regulating fat metabolism or fat metabolic process in subjects, by
PT stabilizing human foreskin fibroblasts alpha in subject, thus regulating
PT fat metabolism or fat metabolic process in subject.
XX
PS Example 9; SEQ ID NO 1; 66pp; English.
XX
CC The invention relates to a novel method for regulating fat metabolism or
CC the fat metabolic process in a subject which comprises stabilising human
CC foreskin fibroblast HIFalpha (hypoxia inducible factor alpha subunit) in
CC the subject, or administering a compound that inhibits HIF hydroxylase
CC activity, thus regulating fat metabolism or the fat metabolic process in
CC the subject. The method of the invention may be useful for regulating fat
CC metabolism or a fat metabolic process in a subject. The subject is an
CC animal, preferably a mammal, more preferably human and the method is
CC performed in a human cell, tissue or organ. The method may be useful for
CC treating or preventing atherosclerosis, diabetes and obesity in a
CC subject. The current sequence is that of the substrate peptide of the
CC invention which is used during a screening assay of human HIF prolyl
CC hydroxylase (HIF-PH).
XX
SQ Sequence 19 AA;

Query Match 62.1%; Score 95; DB 8; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.6e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 16
ADP79479
ID ADP79479 standard; peptide; 19 AA.
XX
AC ADP79479;
XX
DT 04-NOV-2004 (first entry)
XX
DE Hypoxia inducible factor prolyl hydroxylase substrate peptide.
XX
KW Human; Hypoxia inducible factor prolyl hydroxylase; glucose metabolism;
KW antidiabetic; anorectic; hypotensive; antilipaemic; nephrotropic;
KW neuroprotective; ophthalmological; antiarteriosclerotic; vasotropic;
KW enzyme.
XX
OS Homo sapiens.
XX
PN WO2004052284-A2.
XX
PD 24-JUN-2004.
XX
PF 05-DEC-2003; 2003WO-US038689.
XX
PR 06-DEC-2002; 2002US-0431351P.
PR 06-JUN-2003; 2003US-0476331P.
PR 06-JUN-2003; 2003US-0476726P.
PR 04-DEC-2003; 2003US-00729704.
XX
PA (FIBR-) FIBROGEN INC.
XX
PI Guenzler-Pukall V, Klaus SJ, Langsetmo Parobok I, Seeley TW;
XX
DR WPI; 2004-468688/44.
XX
PT Regulating glucose metabolism or glucose metabolic process in subject,
PT involves stabilizing hypoxia inducible factor alpha in subject, or
PT administering to subject compound inhibiting hypoxia inducible factor
PT hydroxylase activity.
XX
PS Example 14; SEQ ID NO 5; 74pp; English.
XX
CC The present sequence is that of a substrate peptide for hypoxia inducible
CC factor (HIF) prolyl hydroxylase. It was used in an example from the
CC invention for the identification of compounds useful for HIF alpha
CC stabilisation. The invention provides methods and compounds for
CC regulating glucose metabolism by stabilising HIF alpha, especially by
CC administering a compound that inhibits HIF hydroxylase activity. The
CC method of stabilising HIF alpha is used in claimed methods for achieving
CC glucose homeostasis, decreasing blood glucose levels, decreasing glycated

```
CC   haemoglobin levels, altering expression of a glucose regulatory factor,
CC   altering expression of a glycolytic factor, treating or preventing
CC   diabetes, treating or preventing a disorder associated with increased
CC   blood glucose levels (especially diabetes, hyperglycaemia, obesity,
CC   hypertension, hyperlipidaemia, nephropathy, neuropathy, retinopathy,
CC   impaired glucose tolerance, atherosclerosis and vascular disease),
CC   treating or preventing a condition associated with diabetes, decreasing
CC   blood triglyceride levels, reducing insulin resistance, and increasing
CC   glycaemic control in a subject.
XX
SQ   Sequence 19 AA;

  Query Match             62.1%;  Score 95;  DB 8;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 3.6e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||||:||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 17
ABP55440
ID   ABP55440 standard; peptide; 20 AA.
XX
AC   ABP55440;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Hypoxia-inducible factor (HIF) 1 alpha peptide.
XX
KW   Hypoxia; hypoxia-inducible factor; HIF1-alpha; hypoxic-related disorder;
KW   ischaemic-related disorder; hypoxia-inducible factor-related disorder;
KW   prolyl hydroxylation; HIF; hypoxic; ischaemic; vasotropic; cardiant;
KW   cerebroprotective; cytostatic; thrombolytic; antidiabetic; nephrotropic;
KW   myocardial infarction; heart disease; stroke; cancer; diabetes;
KW   cell-proliferating disorder; deep vein thrombosis; pulmonary embolus;
KW   renal failure; angiogenesis; vascularisation; prolyl hydroxylase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   9
FT                   /label= hydroxyproline
XX
PN   WO200274249-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US008886.
XX
PR   20-MAR-2001; 2001US-0277425P.
PR   20-MAR-2001; 2001US-0277431P.
PR   20-MAR-2001; 2001US-0277440P.
PR   09-NOV-2001; 2001US-0332334P.
PR   09-NOV-2001; 2001US-0332493P.
PR   09-NOV-2001; 2001US-0345200P.
PR   20-DEC-2001; 2001US-0342598P.
PR   20-DEC-2001; 2001US-0345131P.
PR   20-DEC-2001; 2001US-0345132P.
PR   19-MAR-2002; 2002US-00101812.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Kaelin WG,  Ivan M;
XX
DR   WPI; 2003-058330/05.
XX
PT   Treating or preventing a hypoxic- or ischemic-related disorder, e.g.
PT   myocardial infarction, stroke, cancer, thrombosis or renal failure, by
PT   administering a modulator prolyl hydroxylation of hypoxia-inducible
PT   factor (HIF).
XX
PS   Disclosure; Page 26; 128pp; English.
XX
CC   The present invention describes a method for treating or preventing a
CC   hypoxic-related disorder, ischaemic-related disorder, or hypoxia-
CC   inducible factor (HIF)-related disorder in a subject by administering to
CC   the subject a compound that modulates prolyl hydroxylation of HIF, such
CC   that the hypoxic-, ischaemic-, or HIF-related disorder is treated,
CC   prevented, reversed or stabilised. HIF related sequences can have
CC   vasotropic, cardiant, cerebroprotective, cytostatic, thrombolytic,
CC   antidiabetic, and nephrotropic activities. The method is useful for
CC   treating hypoxia-related disorder, ischaemic-related disorder or HIF-
CC   related disorder. In particular, the hypoxic- or ischaemic-related
CC   disorder is an acute event (e.g. myocardial infarction, heart disease,
CC   stroke, cancer or cell-proliferating disorder, or diabetes) or a chronic
CC   event (e.g. deep vein thrombosis, pulmonary embolus or renal failure),
CC   especially a chronic event not caused by tissue scarring. The method is
CC   also useful for increasing angiogenesis or vascularisation. The present
CC   sequence represents a human hypoxia-inducible factor 1 alpha (HIF1-alpha)
CC   peptide which is given in the exemplification of the present invention
XX
SQ   Sequence 20 AA;

  Query Match             62.1%;  Score 95;  DB 6;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 3.8e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||||:||||||||||
Db          1 DLDLEMLAPYIPMDDDFQL 19


RESULT 18
ADO22337
ID   ADO22337 standard; peptide; 20 AA.
XX
AC   ADO22337;
XX
DT   12-AUG-2004  (first entry)
XX
DE   HIF-1alpha ligand binding site peptide SEQ ID NO:15.
XX
KW   transgenic; transgenic non-human animal; light-generating fusion protein;
KW   ligand binding site; light-generating polypeptide moiety;
KW   hypoxia-inducible factor 1 alpha; HIF-1alpha; hypoxic tissue;
KW   respiratory; cytostatic; vasotropic; virucide; hypoxic condition; cancer;
KW   ischaemia; viral infection; drug screening; drug discovery;
KW   ligand binding site peptide.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004042361-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US035154.
XX
PR   04-NOV-2002; 2002US-00287670.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Kaelin WG,  Livingston DM,  Kim T;
XX
DR   WPI; 2004-400725/37.
XX
PT   New transgenic non-human animal comprising light-generating fusion
PT   protein, useful in diagnosing and treating hypoxic conditions, cancer,
PT   ischemia and viral infections and in drug screening and discovery.
XX
PS   Disclosure; SEQ ID NO 15; 111pp; English.
XX
CC   The present invention describes a transgenic non-human animal comprising
CC   a recombinant nucleic acid molecule stably integrated into the genome of
```

CC the animal, where the molecule encodes a light-generating fusion protein
CC comprising a ligand binding site and a light-generating polypeptide
CC moiety. Also described: (1) an isolated cell of the animal; (2) producing
CC a transgenic non-human animal; (3) identifying a compound capable of
CC modifying an activity of hypoxia-inducible factor (HIF) 1 alpha; and (4)
CC detecting hypoxic tissue. The compound has respiratory, cytostatic,
CC vasotropic and virucide activities. The transgenic non-human animal,
CC light-generating fusion protein, agents, kits and compositions are useful
CC in diagnosing and treating hypoxic conditions, cancer, ischaemia and
CC viral infections and in drug screening and discovery. The present
CC sequence represents a HIF-1alpha ligand binding site peptide, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 20 AA;

Query Match 62.1%; Score 95; DB 8; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.8e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 1 DLDLEMLAPYIPMDDDFQL 19

RESULT 19
AAO23501
ID AAO23501 standard; peptide; 29 AA.
XX
AC AAO23501;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment P563A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 6; Fig 19; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. Sequences AAO23500-509represent mutant fragments
CC within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 29 AA;

Query Match 62.1%; Score 95; DB 7; Length 29;
Best Local Similarity 94.7%; Pred. No. 5.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 10 DLDLEMLAAYIPMDDDFQL 28

RESULT 20
AAO23481
ID AAO23481 standard; peptide; 29 AA.
XX
AC AAO23481;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein mutant fragment.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Claim 39; Page 93; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a specific example
CC of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-

```
CC   related conditions
XX
SQ   Sequence 29 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 29;
  Best Local Similarity   94.7%;  Pred. No. 5.7e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db         10 DLDLEMLAPYIPMDDDFQL 28


RESULT 21
AAO23472
ID   AAO23472 standard; peptide; 29 AA.
XX
AC   AAO23472;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Murine HIF-1alpha protein mutant fragment.
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW   mutant.
XX
OS   Mus sp.
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Claim 39; Page 89; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. The present sequence represents a specific example
CC   of a murine HIF-1 alpha mutant fragment used for treatment for hypoxic-
CC   related conditions
XX
SQ   Sequence 29 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 29;
  Best Local Similarity   94.7%;  Pred. No. 5.7e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db         10 DLDLEMLAAYIPMDDDFQL 28


RESULT 22
AAO23499
ID   AAO23499 standard; peptide; 29 AA.
XX
AC   AAO23499;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Murine HIF-1alpha protein N-TAD region fragment (residues 546-573).
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW   N-TAD.
XX
OS   Mus sp.
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Example 6; Fig 19; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. The present sequence represents a N-TAD region of
CC   a murine HIF-1 alpha protein
XX
SQ   Sequence 29 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 29;
  Best Local Similarity   94.7%;  Pred. No. 5.7e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db         10 DLDLEMLAPYIPMDDDFQL 28
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RESULT 23
AAB49913
ID   AAB49913 standard; peptide; 34 AA.
XX
AC   AAB49913;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Human/murine HIF-1alpha subunit conserved motif #9.
XX
KW   Mouse; human; HIF-1alpha; von Hippel-Lindau syndrome protein; VHL;
KW   hypoxia inducible factor-1; cancer; ischaemia.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO200069908-A1.
XX
PD   23-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-GB001826.
XX
PR   12-MAY-1999;   99GB-00011047.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Ratcliffe PJ,  Maxwell PH,  Pugh CW;
XX
DR   WPI; 2001-025006/03.
XX
PT   Assaying for von Hippel Lindau (VHL)-hypoxia inducible factor (HIF) alpha
PT   subunit interaction modulators for treating ischemia by contacting a VHL
PT   protein and an HIF subunit protein with a putative modulator.
XX
PS   Claim 14; Page 50; 56pp; English.
XX
CC   The present invention describes a novel assay for use in identifying
CC   modulators of the von Hippel-Lindau protein (VHL) and hypoxia inducible
CC   factor-1 alpha subunit (HIF-1alpha) interaction. The assay comprises
CC   contacting the VHL protein, the HIF-1alpha subunit and the putative
CC   modulator under conditions where the former two would normally complex.
CC   Modulators of this type are useful in the treatment of cancer and
CC   ischaemic conditions such as coronary, cerebral and vascular
CC   insufficiency
XX
SQ   Sequence 34 AA;

  Query Match             62.1%;  Score 95;  DB 4;  Length 34;
  Best Local Similarity   94.7%;  Pred. No. 6.8e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db          8 DLDLEMLAPYIPMDDDFQL 26


RESULT 24
AAE30161
ID   AAE30161 standard; peptide; 34 AA.
XX
AC   AAE30161;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Peptide #1 used to block HIF-1alpha/pVHL interaction.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Maxwell PH,  Pugh CW,  Ratcliffe PJ,  Schofield CJ;
XX
DR   WPI; 2003-018808/01.
XX
PT   Novel isolated polypeptide useful for treating ischemia, wound healing,
PT   auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT   cancer, or inflammatory disorders.
XX
PS   Example 1; Page 246; 256pp; English.
XX
CC   The invention relates to polypeptides having hypoxia inducible factor
CC   (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC   3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC   the invention are used for treating conditions such as ischaemia, wound
CC   healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC   pressure, cancer, or inflammatory disorders. They are useful in anti-
CC   sense regulation of the HIF hydroxylase activity and in particular HIF
CC   prolyl hydroxylase activity within a cell. They are also used to identify
CC   additional substrates of HIF hydroxylases. Sequences of the invention are
CC   used to design double stranded RNAs for use in RNA interference. They are
CC   used as therapeutic agents and in purification, isolation, or screening
CC   methods involving immuno- precipitation techniques and for detecting
CC   polypeptides in biological samples. The invention is useful in gene
CC   therapy. The present sequence is a peptide used to block HIF-1alpha/pVHL
CC   interaction. This sequence is used in the invention
XX
SQ   Sequence 34 AA;

  Query Match             62.1%;  Score 95;  DB 6;  Length 34;
  Best Local Similarity   94.7%;  Pred. No. 6.8e-06;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db          8 DLDLEMLAPYIPMDDDFQL 26


RESULT 25
AAE30151
ID   AAE30151 standard; peptide; 34 AA.
XX
AC   AAE30151;
XX
DT   24-FEB-2003  (first entry)
XX
DE   HIFalpha subunit antagonist #8.
XX
KW   Hypoxia inducible factor; HIF hydroxylase; inflammatory disorder; cancer;
KW   wound healing; ischaemia; transplantation; blood pressure; gene therapy;
KW   antagonist.
XX
OS   Unidentified.
XX
PN   WO200274981-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-GB001381.
XX
PR   21-MAR-2001; 2001GB-00007123.
PR   02-AUG-2001; 2001GB-00018952.
XX
```

PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Maxwell PH, Pugh CW, Ratcliffe PJ, Schofield CJ;
XX
DR WPI; 2003-018808/01.
XX
PT Novel isolated polypeptide useful for treating ischemia, wound healing,
PT auto-, allo-, and xeno-transplantation, systemic high blood pressure,
PT cancer, or inflammatory disorders.
XX
PS Disclosure; Page 239; 256pp; English.
XX
CC The invention relates to polypeptides having hypoxia inducible factor
CC (HIF) hydroxylase activity, referred to as PHD polypeptides (PHD 1,2 and
CC 3) and nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are used for treating conditions such as ischaemia, wound
CC healing, auto-, allo-, and xeno-transplantation, systemic high blood
CC pressure, cancer, or inflammatory disorders. They are useful in anti-
CC sense regulation of the HIF hydroxylase activity and in particular HIF
CC prolyl hydroxylase activity within a cell. They are also used to identify
CC additional substrates of HIF hydroxylases. Sequences of the invention are
CC used to design double stranded RNAs for use in RNA interference. They are
CC used as therapeutic agents and in purification, isolation, or screening
CC methods involving immuno- precipitation techniques and for detecting
CC polypeptides in biological samples. The invention is useful in gene
CC therapy. The present sequence is HIFalpha subunit antagonist. This
CC sequence is used in the invention
XX
SQ Sequence 34 AA;

Query Match 62.1%; Score 95; DB 6; Length 34;
Best Local Similarity 94.7%; Pred. No. 6.8e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 8 DLDLEMLAPYIPMDDDFQL 26

RESULT 26
AAY94637
ID AAY94637 standard; protein; 54 AA.
XX
AC AAY94637;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/531-584.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 19; Page 84-85; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 54 AA;

Query Match 62.1%; Score 95; DB 3; Length 54;
Best Local Similarity 94.7%; Pred. No. 1.1e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 26 DLDLEMLAPYIPMDDDFQL 44

RESULT 27
AAO23490
ID AAO23490 standard; peptide; 54 AA.
XX
AC AAO23490;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region fragment (residues 531-584).
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 4; Fig 4; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability

CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. The present sequence represents a N-TAD region of
CC a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 62.1%; Score 95; DB 7; Length 54;
Best Local Similarity 94.7%; Pred. No. 1.1e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 28
AAO23530
ID AAO23530 standard; peptide; 54 AA.
XX
AC AAO23530;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment Q572A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 11; Fig 27; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of
CC cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ Sequence 54 AA;

Query Match 62.1%; Score 95; DB 7; Length 54;
Best Local Similarity 94.7%; Pred. No. 1.1e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 25 DLDLEMLAPYIPMDDDFQL 43

RESULT 29
AAO23528
ID AAO23528 standard; peptide; 54 AA.
XX
AC AAO23528;
XX
DT 12-FEB-2004 (first entry)
XX
DE Murine HIF-1alpha protein N-TAD region mutant fragment L573A.
XX
KW HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW N-TAD; mutant.
XX
OS Mus sp.
XX
PN WO2003074560-A2.
XX
PD 12-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-SE000372.
XX
PR 05-MAR-2002; 2002US-0361333P.
PR 27-NOV-2002; 2002US-0429307P.
XX
PA (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI Pereira T, Poellinger L, Hellstroem M;
XX
DR WPI; 2003-712876/67.
XX
PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT angiogenesis, or treating a condition associated with HIF-1alpha
PT underexpression in a cell, a group of cells, or an organism, e.g.
PT ischemia or inflammation.
XX
PS Example 11; Fig 27; 96pp; English.
XX
CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC that has (a) an altered transactivation capacity and improved stability
CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC pharmaceutical composition are useful for increasing angiogenesis,
CC interfering with a normal response to reoxygenation following hypoxia, or
CC treating a condition associated with HIF-1alpha underexpression in a
CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC stroke. The proteins and pharmaceutical compositions are also useful for
CC mimicking the hypoxic response or artificially inducing a hypoxic
CC response in a cell, group of cells, or organism, inducing vascular
CC formation or vascular development in a cell or a group of cells,
CC increasing angiogenetic activity in a cell, or influencing erythropoietin
CC production, metabolism, or an inflammatory response in a cell, a group of

```
CC   cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC   within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ   Sequence 54 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 54;
  Best Local Similarity   94.7%;  Pred. No. 1.1e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db         25 DLDLEMLAPYIPMDDDFQL 43


RESULT 30
AAO23519
ID   AAO23519 standard; peptide; 54 AA.
XX
AC   AAO23519;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Murine HIF-1alpha protein N-TAD region mutant fragment P563A.
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW   N-TAD; mutant.
XX
OS   Mus sp.
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Example 11; Fig 27; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC   within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ   Sequence 54 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 54;
  Best Local Similarity   94.7%;  Pred. No. 1.1e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db         25 DLDLEMLAAYIPMDDDFQL 43


RESULT 31
AAO23529
ID   AAO23529 standard; peptide; 54 AA.
XX
AC   AAO23529;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Murine HIF-1alpha protein N-TAD region mutant fragment QR-A.
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW   N-TAD; mutant.
XX
OS   Mus sp.
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Example 11; Fig 27; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. Sequences AAO23518-30 represent mutant fragments
CC   within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ   Sequence 54 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 54;
  Best Local Similarity   94.7%;  Pred. No. 1.1e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db         25 DLDLEMLAPYIPMDDDFQL 43
```

```
RESULT 32
AAO23493
ID   AAO23493 standard; peptide; 54 AA.
XX
AC   AAO23493;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Murine HIF-1alpha protein N-TAD region mutant fragment P-A.
XX
KW   HIF-1alpha; hypoxia-inducible factor -1alpha; vasotropic; antidiabetic;
KW   ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;
KW   antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;
KW   N-TAD; mutant.
XX
OS   Mus sp.
XX
PN   WO2003074560-A2.
XX
PD   12-SEP-2003.
XX
PF   05-MAR-2003; 2003WO-SE000372.
XX
PR   05-MAR-2002; 2002US-0361333P.
PR   27-NOV-2002; 2002US-0429307P.
XX
PA   (ANGI-) ANGIOGENETICS SWEDEN AB.
XX
PI   Pereira T,  Poellinger L,  Hellstroem M;
XX
DR   WPI; 2003-712876/67.
XX
PT   New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
PT   angiogenesis, or treating a condition associated with HIF-1alpha
PT   underexpression in a cell, a group of cells, or an organism, e.g.
PT   ischemia or inflammation.
XX
PS   Example 4; Fig 4; 96pp; English.
XX
CC   The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
CC   that has (a) an altered transactivation capacity and improved stability
CC   at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
CC   pharmaceutical composition are useful for increasing angiogenesis,
CC   interfering with a normal response to reoxygenation following hypoxia, or
CC   treating a condition associated with HIF-1alpha underexpression in a
CC   cell, a group of cells, or an organism, e.g. ischaemia, diabetic
CC   retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
CC   stroke. The proteins and pharmaceutical compositions are also useful for
CC   mimicking the hypoxic response or artificially inducing a hypoxic
CC   response in a cell, group of cells, or organism, inducing vascular
CC   formation or vascular development in a cell or a group of cells,
CC   increasing angiogenetic activity in a cell, or influencing erythropoietin
CC   production, metabolism, or an inflammatory response in a cell, a group of
CC   cells, or an organism. Sequences AAO23491-98 represent mutant fragments
CC   within the N-TAD region of a murine HIF-1 alpha protein
XX
SQ   Sequence 54 AA;

  Query Match             62.1%;  Score 95;  DB 7;  Length 54;
  Best Local Similarity   94.7%;  Pred. No. 1.1e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db         25 DLDLEMLAAYIPMDDDFQL 43


RESULT 33
AAY94632
ID   AAY94632 standard; protein; 116 AA.
XX
AC   AAY94632;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/526-641.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS   Homo sapiens.
XX
PN   WO200029437-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-SE002053.
XX
PR   13-NOV-1998;   98SE-00003891.
XX
PA   (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI   Berkenstam A,  Poellinger L;
XX
DR   WPI; 2000-399715/34.
XX
PT   Human hypoxia-inducible factor alpha variants for identifying compounds
PT   that modulate its functional domain and regulate genes involved in
PT   angiogenesis, erythropoiesis.
XX
PS   Claim 13; Page 76-77; 87pp; English.
XX
CC   This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC   -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC   multi-step process which includes hypoxia-dependent nuclear import and
CC   activation of the transactivation domain. The HIF-1alpha consists of a
CC   number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC   located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC   nuclear localization sequence located at amino acids 718-584, a
CC   transactivator domain (N-TAD) located between amino acids 531 and 584,
CC   and a second transactivator domain (C-TAD) located between 813 and 826.
CC   The invention relates to isolated variants of HIF-1alpha, such as that
CC   represented by the present sequence. The variants are useful for
CC   identifying compounds capable of modulating the function of a functional
CC   domain of human HIF-1alpha. The method comprises contacting a candidate
CC   compound with a cell expressing a HIF-1alpha variant conjugated to a
CC   molecular probe. The localization of the probe can be detected in the
CC   cell. The Aequeora victoria green fluorescent protein can be used as the
CC   molecular probe. The compounds are useful for the regulation of HIF-
CC   1alpha target genes, such as those involved in the regulation of
CC   angiogenesis, erythropoiesis an glycolysis
XX
SQ   Sequence 116 AA;

  Query Match             62.1%;  Score 95;  DB 3;  Length 116;
  Best Local Similarity   94.7%;  Pred. No. 2.6e-05;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db         31 DLDLEMLAPYIPMDDDFQL 49


RESULT 34
AAY94633
ID   AAY94633 standard; protein; 288 AA.
XX
AC   AAY94633;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/526-813.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
```

KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 77-78; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 288 AA;

Query Match 62.1%; Score 95; DB 3; Length 288;
Best Local Similarity 94.7%; Pred. No. 7e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 35
AAY94634
ID AAY94634 standard; protein; 301 AA.
XX
AC AAY94634;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/526-826.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 78-79; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 301 AA;

Query Match 62.1%; Score 95; DB 3; Length 301;
Best Local Similarity 94.7%; Pred. No. 7.3e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 31 DLDLEMLAPYIPMDDDFQL 49

RESULT 36
AAY94631
ID AAY94631 standard; protein; 311 AA.
XX
AC AAY94631;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/331-641.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX

PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 74-75; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 311 AA;

Query Match 62.1%; Score 95; DB 3; Length 311;
Best Local Similarity 94.7%; Pred. No. 7.6e-05;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 226 DLDLEMLAPYIPMDDDFQL 244

RESULT 37
ADO39389
ID ADO39389 standard; protein; 409 AA.
XX
AC ADO39389;
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #3.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39384.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
PS Disclosure; Fig 6H; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 409 AA;

Query Match 62.1%; Score 95; DB 8; Length 409;
Best Local Similarity 94.7%; Pred. No. 0.0001;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 38
AAB68415
ID AAB68415 standard; protein; 444 AA.
XX
AC AAB68415;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of tTAk-hH104.
XX
KW Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
KW anemia; cancer; ischemia; erythropoietin; immunotherapy;
KW autoimmune disease; hH104; tTAk.
XX
OS Synthetic.
XX
PN WO200136616-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-FR003207.
XX
PR 18-NOV-1999; 99FR-00014513.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (AVET) AVENTIS PHARMA SA.
XX
PI Beuzard Y, Payen E, Scherman D, Bettan M;
XX
DR WPI; 2001-343818/36.
DR N-PSDB; AAF85323.

XX
PT New nucleic acid construct for controlling expression of target gene,
PT useful e.g. for treating cancer, is modulated by exogeneous
PT pharmaceutical and oxygen partial pressure.
XX
PS Disclosure; Page 57-58; 60pp; French.
XX
CC The specification describes a nucleic acid construct bearing a system for
CC regulating the expression of a gene. The nucleic acid construct comprises
CC at least one sequence encoding a protein that regulates expression of at
CC least one gene of interest. The activity of this protein is modulated by
CC presence/absence of a pharmacological agent and the amount of protein
CC produced depends on the oxygen partial pressure. The constructs are used
CC to treat conditions associated with cellular hypoxia, especially anemia,
CC cancer and ischemia, specifically where the gene of interest encodes
CC erythropoietin (but many other suitable genes are listed, e.g. those
CC encoding single-chain antibodies for immunotherapy of infections or
CC autoimmune diseases, prodrug-converting enzymes, apoptosis inducers
CC etc.). The present sequence is encoded by the open reading frame of tTAk-
CC hH104. The sequence contains a human hH104 fragment, inserted into the
CC BsiWI site of tTAk. The sequence is used to produce constructs of the
CC invention
XX
SQ Sequence 444 AA;

Query Match 62.1%; Score 95; DB 4; Length 444;
Best Local Similarity 94.7%; Pred. No. 0.00011;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 242 DLDLEMLAPYIPMDDDFQL 260

RESULT 39
ADO39390
ID ADO39390 standard; protein; 466 AA.
XX
AC ADO39390;
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #4.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39385.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
PS Disclosure; Fig 6I; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 466 AA;

Query Match 62.1%; Score 95; DB 8; Length 466;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 235 DLDLEMLAPYIPMDDDFQL 253

RESULT 40
ADO39387
ID ADO39387 standard; protein; 538 AA.
XX
AC ADO39387;
XX
DT 15-JUL-2004 (first entry)
XX
DE Chimeric transactivator THV fragment #1.
XX
KW haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW tetracycline resistance; VP16.
XX
OS Homo sapiens.
XX
PN US2004018606-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00425833.
XX
PR 30-APR-2002; 2002US-0376269P.
XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39382.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX

```
PS   Disclosure; Fig 6F; 28pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which codes for a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions. Also described are: a chimeric transactivator comprising a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions; an isolated polynucleotide which codes for the chimeric
CC   transactivator (1); a vector comprising the chimeric transactivator
CC   polynucleotide (2); a composition comprising polynucleotide (2) and a
CC   polynucleotide which contains a sequence that codes for a target gene and
CC   a promoter which is regulated by the chimeric transactivator coded; a
CC   method of expressing a target gene in a subject, comprising administering
CC   the composition of (4); a method of increasing the number of red blood
CC   cells in a subject, comprising administering the composition of (4) to
CC   the subject; and a method of increasing the number of blood vessels in
CC   subject, comprising administering the composition of (4) to the subject.
CC   The methods and compositions of the present invention are useful for
CC   treating anaemia associated with AIDS or cancer, anaemia from
CC   inflammatory origin and haemoglobinopathies. This is the amino acid
CC   sequence of a fragment of a chimeric transactivator comprising regions of
CC   the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC   transcription factor gene and VP16.
XX
SQ   Sequence 538 AA;

  Query Match             62.1%;  Score 95;  DB 8;  Length 538;
  Best Local Similarity   94.7%;  Pred. No. 0.00014;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        364 DLDLEMLAPYIPMDDDFQL 382


RESULT 41
ABP41474
ID   ABP41474 standard; protein; 542 AA.
XX
AC   ABP41474;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Human ovarian antigen HNORJ10, SEQ ID NO:2606.
XX
KW   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW   ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW   infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW   PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW   inflammatory condition; immune disorder; blood disorder;
KW   cardiovascular disorder; respiratory disorder; neurological disorder;
KW   gastrointestinal disorder; urinary system disorder; drug screening;
KW   gene therapy; chromosome mapping; forensic analysis;
KW   antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW   antiinflammatory; gynaecological; reproductive; chromosome 14q21-24.
XX
OS   Homo sapiens.
XX
PN   WO200200677-A1.
XX
PD   03-JAN-2002.
XX
PF   07-JUN-2001; 2001WO-US018569.
XX
PR   07-JUN-2000; 2000US-0209467P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE,  Rosen CA;
XX
DR   WPI; 2002-147878/19.
DR   N-PSDB; ABQ54551.
XX
PT   Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT   useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT   cancer), immune disorders, cardiovascular disorders and neurological
PT   diseases.
XX
PS   Claim 11; SEQ ID NO 2606; 2922pp; English.
XX
CC   The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC   ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC   encompasses polypeptides 90% identical and polynucleotides 95% identical
CC   to the sequences of the invention. The invention additionally relates to
CC   recombinant vectors and host cells comprising human ovarian antigen
CC   polynucleotides, antibodies against human ovarian antigens, and the use
CC   of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC   treating, prognosing or preventing various ovary and/or breast-related
CC   disorders. Such conditions include ovarian cancer and breast cancer, and
CC   metastatic tumours of ovarian or breast origin, reproductive system
CC   disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC   polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC   disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC   shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC   vaginitis), immune disorders (e.g., congenital and acquired
CC   immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC   blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC   respiratory disorders, neurological disorders, gastrointestinal disorders
CC   and urinary system disorders. Ovarian antigen polypeptides and
CC   polynucleotides may also be used in screening for compounds which
CC   modulate ovarian antigen expression or activity. The polynucleotides may
CC   further be used for gene therapy, chromosome mapping, in the
CC   identification of individuals and in forensic analysis, and the
CC   polypeptides may be used as food additives or to prepare antibodies
CC   useful in disease diagnosis, drug targeting and phenotyping. The present
CC   sequence represents a human ovarian antigen of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 542 AA;

  Query Match             62.1%;  Score 95;  DB 5;  Length 542;
  Best Local Similarity   94.7%;  Pred. No. 0.00014;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        272 DLDLEMLAPYIPMDDDFQL 290


RESULT 42
ADO39388
ID   ADO39388 standard; protein; 595 AA.
XX
AC   ADO39388;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Chimeric transactivator THV fragment #2.
XX
KW   haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW   normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW   inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW   tetracycline resistance; VP16.
XX
OS   Homo sapiens.
XX
PN   US2004018606-A1.
XX
PD   29-JAN-2004.
XX
PF   30-APR-2003; 2003US-00425833.
XX
PR   30-APR-2002; 2002US-0376269P.
```

XX
PA (BOHL/) BOHL D.
PA (HEAR/) HEARD M.
XX
PI Bohl D, Heard M;
XX
DR WPI; 2004-122040/12.
DR N-PSDB; ADO39383.
XX
PT New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT of a transcription factor susceptible to degradation under normoxia
PT conditions, useful for treating anemia associated with AIDS, cancer and
PT inflammation.
XX
PS Disclosure; Fig 6G; 28pp; English.
XX
CC The invention describes an isolated polynucleotide (I) which codes for a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions. Also described are: a chimeric transactivator comprising a
CC domain of a transcription factor, wherein the domain confers to the
CC transcription factor susceptibility to degradation under normoxia
CC conditions; an isolated polynucleotide which codes for the chimeric
CC transactivator (1); a vector comprising the chimeric transactivator
CC polynucleotide (2); a composition comprising polynucleotide (2) and a
CC polynucleotide which contains a sequence that codes for a target gene and
CC a promoter which is regulated by the chimeric transactivator coded; a
CC method of expressing a target gene in a subject, comprising administering
CC the composition of (4); a method of increasing the number of red blood
CC cells in a subject, comprising administering the composition of (4) to
CC the subject; and a method of increasing the number of blood vessels in
CC subject, comprising administering the composition of (4) to the subject.
CC The methods and compositions of the present invention are useful for
CC treating anaemia associated with AIDS or cancer, anaemia from
CC inflammatory origin and haemoglobinopathies. This is the amino acid
CC sequence of a fragment of a chimeric transactivator comprising regions of
CC the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC transcription factor gene and VP16.
XX
SQ Sequence 595 AA;

Query Match 62.1%; Score 95; DB 8; Length 595;
Best Local Similarity 94.7%; Pred. No. 0.00015;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 364 DLDLEMLAPYIPMDDDFQL 382

RESULT 43
AAY94630
ID AAY94630 standard; protein; 613 AA.
XX
AC AAY94630;
XX
DT 15-AUG-2000 (first entry)
XX
DE HIF-1alpha variant protein sequence HIF-1alpha/delta178-390.
XX
KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS Homo sapiens.
XX
PN WO200029437-A1.
XX
PD 25-MAY-2000.
XX
PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 13; Page 72-74; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 613 AA;

Query Match 62.1%; Score 95; DB 3; Length 613;
Best Local Similarity 94.7%; Pred. No. 0.00016;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 343 DLDLEMLAPYIPMDDDFQL 361

RESULT 44
AAU77614
ID AAU77614 standard; protein; 613 AA.
XX
AC AAU77614;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human hypoxia-inducible factor-1 alpha, HIF-1, mutant delta 178-390.
XX
KW Human; HIF-1; hypoxia-inducible factor-1; rheumatoid arthritis;
KW transactivation domain; N-TAD; C-TAD; ischaemia; brain infarction;
KW circulatory disorder; cancer; hypertension; demyelinating disorder;
KW angiogenesis; sarcoidosis; hepatitis-caused inflammation;
KW chronic ulceration; neovascularisation; arterial hypervascularisation;
KW bullous skin disease; vasculitis; dermatomyositis; polymyositis; mutant;
KW mutein; Y565G.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 177. .178
FT /note= "Residues 178-390 of the wild-type HIF-1 have been
FT deleted"
XX
PN WO200212326-A2.
XX
PD 14-FEB-2002.
XX

```
PF   07-AUG-2001; 2001WO-IB001775.
XX
PR   07-AUG-2000; 2000US-0223480P.
XX
PA   (ASPE-) ASPERA PHARM AB.
XX
PI   Poellinger L,  Pereira T,  Ruas J;
XX
DR   WPI; 2002-257466/30.
XX
PT   New polypeptides comprising hypoxia-inducible factor-1 with alterations
PT   of the transactivation domain, useful treating ischemic conditions, e.g.
PT   brain infarction, heart infarction or circulatory disorder.
XX
PS   Example 5; Page; 80pp; English.
XX
CC   The invention relates to a polypeptide comprising hypoxia-inducible
CC   factor-1 (HIF-1) with alterations of the transactivation domain (N-TAD or
CC   C-TAD). Also included are nucleic acids encoding the altered proteins, a
CC   vector comprising the nucleic acid, a host cell transformed with the
CC   vector, methods for producing the protein or its functional fragment or
CC   an isolated degradation box, a method of screening for an agent that
CC   modulates N-TAD function and antagonists, agonists, modulators and HIF-1
CC   peptide fragments useful for modulating HIF-1 function or the function of
CC   proteins that interact with it. The isolated polypeptides and their
CC   fragments with altered residues are useful in methods for treating
CC   diseases. The disease is an ischaemic condition, e.g. brain infarction,
CC   heart infarction or circulatory disorder. The disease may also be cancer,
CC   hypertension, demyelinating disorders, diffuse proliferative
CC   glomerulonephritis, toxoplasmosis caused retinochorioiditis, HIV (human
CC   immunodeficiency virus) caused Tat angiogenesis, HIV-caused Kaposi's
CC   sarcoma, hepatitis-caused inflammation, hepatitis-caused angiogenesis,
CC   chronic ulceration, proliferative retinopathy, retina haemangioblastomas,
CC   neovascularisation, arterial hypervascularisation, sarcoidosis, bullous
CC   skin disease, vasculitis with angiogenesis, dermatomyositis with
CC   angiogenesis, polymyositis with angiogenesis, rheumatoid arthritis,
CC   juvenile osteoarthritis, polyarthritis, aneurysm or atheroma. The present
CC   sequence represents HIF-1 mutant delta 178-390. Note: The present
CC   sequence is not shown in the specification but was created by the indexer
CC   using the information in example 5 and the HIF sequence appearing as
CC   AAU77602
XX
SQ   Sequence 613 AA;

  Query Match             62.1%;  Score 95;  DB 5;  Length 613;
  Best Local Similarity   94.7%;  Pred. No. 0.00016;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        343 DLDLEMLAPYIPMDDDFQL 361


RESULT 45
ADO39391
ID   ADO39391 standard; protein; 632 AA.
XX
AC   ADO39391;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Chimeric transactivator THV fragment #5.
XX
KW   haemostatic; vasotropic; erythropoietin-agonist; transcription factor;
KW   normoxia; transcription factor degradation; anaemia; AIDS; cancer;
KW   inflammatory; haemoglobinopathy; mouse; hypoxia-inducaed factor 1; HIF-1;
KW   tetracycline resistance; VP16.
XX
OS   Homo sapiens.
XX
PN   US2004018606-A1.
XX
PD   29-JAN-2004.
XX
PF   30-APR-2003; 2003US-00425833.
XX
PR   30-APR-2002; 2002US-0376269P.
XX
PA   (BOHL/) BOHL D.
PA   (HEAR/) HEARD M.
XX
PI   Bohl D,  Heard M;
XX
DR   WPI; 2004-122040/12.
DR   N-PSDB; ADO39386.
XX
PT   New hypoxia-induced factor (HIF) isolated polynucleotide coding a domain
PT   of a transcription factor susceptible to degradation under normoxia
PT   conditions, useful for treating anemia associated with AIDS, cancer and
PT   inflammation.
XX
PS   Disclosure; Fig 6J; 28pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which codes for a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions. Also described are: a chimeric transactivator comprising a
CC   domain of a transcription factor, wherein the domain confers to the
CC   transcription factor susceptibility to degradation under normoxia
CC   conditions; an isolated polynucleotide which codes for the chimeric
CC   transactivator (1); a vector comprising the chimeric transactivator
CC   polynucleotide (2); a composition comprising polynucleotide (2) and a
CC   polynucleotide which contains a sequence that codes for a target gene and
CC   a promoter which is regulated by the chimeric transactivator coded; a
CC   method of expressing a target gene in a subject, comprising administering
CC   the composition of (4); a method of increasing the number of red blood
CC   cells in a subject, comprising administering the composition of (4) to
CC   the subject; and a method of increasing the number of blood vessels in
CC   subject, comprising administering the composition of (4) to the subject.
CC   The methods and compositions of the present invention are useful for
CC   treating anaemia associated with AIDS or cancer, anaemia from
CC   inflammatory origin and haemoglobinopathies. This is the amino acid
CC   sequence of a fragment of a chimeric transactivator comprising regions of
CC   the tetracycline resistance gene, mouse hypoxia-induced factor 1 (HIF-1)
CC   transcription factor gene and VP16.
XX
SQ   Sequence 632 AA;

  Query Match             62.1%;  Score 95;  DB 8;  Length 632;
  Best Local Similarity   94.7%;  Pred. No. 0.00016;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        235 DLDLEMLAPYIPMDDDFQL 253


RESULT 46
AAY94629
ID   AAY94629 standard; protein; 652 AA.
XX
AC   AAY94629;
XX
DT   15-AUG-2000  (first entry)
XX
DE   HIF-1alpha variant protein sequence HIF-1alpha/1-652.
XX
KW   Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD;
KW   regulation; angiogenesis; erythropoiesis; glycolysis; human.
XX
OS   Homo sapiens.
XX
PN   WO200029437-A1.
XX
PD   25-MAY-2000.
XX
```

PF 11-NOV-1999; 99WO-SE002053.
XX
PR 13-NOV-1998; 98SE-00003891.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Poellinger L;
XX
DR WPI; 2000-399715/34.
XX
PT Human hypoxia-inducible factor alpha variants for identifying compounds
PT that modulate its functional domain and regulate genes involved in
PT angiogenesis, erythropoiesis.
XX
PS Claim 15; Page 69-70; 87pp; English.
XX
CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
CC multi-step process which includes hypoxia-dependent nuclear import and
CC activation of the transactivation domain. The HIF-1alpha consists of a
CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
CC nuclear localization sequence located at amino acids 718-584, a
CC transactivator domain (N-TAD) located between amino acids 531 and 584,
CC and a second transactivator domain (C-TAD) located between 813 and 826.
CC The invention relates to isolated variants of HIF-1alpha, such as that
CC represented by the present sequence. The variants are useful for
CC identifying compounds capable of modulating the function of a functional
CC domain of human HIF-1alpha. The method comprises contacting a candidate
CC compound with a cell expressing a HIF-1alpha variant conjugated to a
CC molecular probe. The localization of the probe can be detected in the
CC cell. The Aequeora victoria green fluorescent protein can be used as the
CC molecular probe. The compounds are useful for the regulation of HIF-
CC 1alpha target genes, such as those involved in the regulation of
CC angiogenesis, erythropoiesis an glycolysis
XX
SQ Sequence 652 AA;

Query Match 62.1%; Score 95; DB 3; Length 652;
Best Local Similarity 94.7%; Pred. No. 0.00017;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 556 DLDLEMLAPYIPMDDDFQL 574

RESULT 47
AAY84167
ID AAY84167 standard; protein; 669 AA.
XX
AC AAY84167;
XX
DT 03-JUL-2000 (first entry)
XX
DE A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200010578-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019416.
XX
PR 25-AUG-1998; 98US-00148547.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Semenza GL;
XX
DR WPI; 2000-246493/21.
XX
PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.
XX
PS Claim 1; Page; 96pp; English.
XX
CC The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 549-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They is also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 669 AA;

Query Match 62.1%; Score 95; DB 3; Length 669;
Best Local Similarity 94.7%; Pred. No. 0.00017;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 DLDLEMLAXYIPMDDDFQL 30
||||||||:||||||||||
Db 399 DLDLEMLAPYIPMDDDFQL 417

RESULT 48
AAY84166
ID AAY84166 standard; protein; 697 AA.
XX
AC AAY84166;
XX
DT 03-JUL-2000 (first entry)
XX
DE A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW ischemia related damage; angiogenesis; coronary artery disease;
KW ischemic tissue damage.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 422
FT /note= "this residue is optionally not Ser, and is
FT preferably Gly"
FT Misc-difference 423
FT /note= "this residue is optionally not Thr, and is
FT preferably Ala"
XX
PN WO200010578-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019416.
XX
PR 25-AUG-1998; 98US-00148547.
XX

```
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 521-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 697 AA;

  Query Match             62.1%;  Score 95;  DB 3;  Length 697;
  Best Local Similarity   94.7%;  Pred. No. 0.00018;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        427 DLDLEMLAPYIPMDDDFQL 445


RESULT 49
AAY84173
ID   AAY84173 standard; protein; 701 AA.
XX
AC   AAY84173;
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 426
FT                   /note= "this residue is not Ser, and is preferably Gly"
FT   Misc-difference 427
FT                   /note= "this residue is not Thr, and is preferably Ala"
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
DR   WPI; 2000-246493/21.
XX
PT   Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT   treating hypoxia or ischemia-related tissue damage.
XX
PS   Claim 1; Page; 96pp; English.
XX
CC   The present sequence represents a variant of hypoxia-inducible factor
CC   (HIF)-1 alpha, comprising amino acids 1-391 and 517-826 of the wild type
CC   protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC   and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC   391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC   512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC   which residues 551 and 552 are not serine and threonine, respectively.
CC   The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC   expression of a hypoxia inducible gene in a cell. They is also useful for
CC   providing constitutive expression of a hypoxia inducible factor in a
CC   cell, and for reducing or preventing hypoxia or ischemia related damage.
CC   The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC   therapy for inducing the level of angiogenesis in tissues of patients at
CC   risk of coronary artery disease or ischemic tissue damage. note: this
CC   sequence does not appear in the specification; it was created using
CC   information provided
XX
SQ   Sequence 701 AA;

  Query Match             62.1%;  Score 95;  DB 3;  Length 701;
  Best Local Similarity   94.7%;  Pred. No. 0.00018;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        431 DLDLEMLAPYIPMDDDFQL 449


RESULT 50
AAY84172
ID   AAY84172 standard; protein; 710 AA.
XX
AC   AAY84172;
XX
DT   03-JUL-2000  (first entry)
XX
DE   A variant of human hypoxia inducible factor-1 alpha protein.
XX
KW   Human; hypoxia-inducible factor 1 alpha; HIF-1alpha; variant;
KW   hypoxia inducible gene; hypoxia inducible factor; hypoxia;
KW   ischemia related damage; angiogenesis; coronary artery disease;
KW   ischemic tissue damage.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 435
FT                   /note= "this residue is not Ser, and is preferably Gly"
FT   Misc-difference 436
FT                   /note= "this residue is not Thr, and is preferably Ala"
XX
PN   WO200010578-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019416.
XX
PR   25-AUG-1998;   98US-00148547.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Semenza GL;
XX
```

DR WPI; 2000-246493/21.
XX
PT Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
PT treating hypoxia or ischemia-related tissue damage.
XX
PS Claim 1; Page; 96pp; English.
XX
CC The present sequence represents a variant of hypoxia-inducible factor
CC (HIF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild type
CC protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic
CC and non-hypoxic conditions. The variants comprises amino acid residues 1-
CC 391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826,
CC 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in
CC which residues 551 and 552 are not serine and threonine, respectively.
CC The HIF-1alpha variant polynucleotide sequences are useful for increasing
CC expression of a hypoxia inducible gene in a cell. They is also useful for
CC providing constitutive expression of a hypoxia inducible factor in a
CC cell, and for reducing or preventing hypoxia or ischemia related damage.
CC The variant HIF-1alpha polypeptides are useful for providing prophylactic
CC therapy for inducing the level of angiogenesis in tissues of patients at
CC risk of coronary artery disease or ischemic tissue damage. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 710 AA;

Query Match 62.1%; Score 95; DB 3; Length 710;
Best Local Similarity 94.7%; Pred. No. 0.00019;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        440 DLDLEMLAPYIPMDDDFQL 458
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Search completed: February 8, 2005, 20:15:10
Job time : 161.526 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 19:39:04 ; Search time 148.947 Seconds
(without alignments)
103.140 Million cell updates/sec

Title: US-10-032-361-7
Perfect score: 153
Sequence: 1 YGRKKRRQRRRDLDLEMLAXYIPMDDDFQL 30

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98	64.1	766	1	HIFA_ONCMY	Q98sw2 oncorhynchu
2	97	63.4	777	2	Q6EHI4	Q6ehi4 brachydanio
3	96	62.7	774	2	Q6STN7	Q6stn7 ctenopharyn
4	95	62.1	786	2	Q6SLL1	Q6sll1 canis famil
5	95	62.1	802	2	Q6PI54	Q6pi54 xenopus lae
6	95	62.1	805	1	HIFA_XENLA	Q9i8a9 xenopus lae
7	95	62.1	811	1	HIFA_CHICK	Q9yib9 gallus gall
8	95	62.1	819	2	Q7YSE5	Q7yse5 oryctolagus
9	95	62.1	821	2	Q64F54	Q64f54 spermophilu
10	95	62.1	823	1	HIFA_BOVIN	Q9xta5 bos taurus
11	95	62.1	823	2	Q6IV47	Q6iv47 bos mutus g
12	95	62.1	824	2	Q6H8T3	Q6h8t3 spalax juda
13	95	62.1	825	1	HIFA_RAT	O35800 rattus norv
14	95	62.1	826	1	HIFA_HUMAN	Q16665 homo sapien
15	95	62.1	836	1	HIFA_MOUSE	Q61221 mus musculu
16	81	52.9	630	2	Q9QX54	Q9qx54 mus musculu
17	81	52.9	632	2	Q8WXA1	Q8wxa1 homo sapien
18	81	52.9	643	2	Q6STN6	Q6stn6 ctenopharyn
19	81	52.9	648	2	Q9HAI2	Q9hai2 homo sapien
20	81	52.9	662	2	Q9Z2I5	Q9z2i5 mus musculu
21	81	52.9	667	2	Q9Y2N7	Q9y2n7 homo sapien
22	81	52.9	669	2	Q66K72	Q66k72 homo sapien
23	80	52.3	571	2	Q7T2E4	Q7t2e4 brachydanio
24	80	52.3	626	2	Q6EGR9	Q6egr9 brachydanio
25	78.5	51.3	662	2	Q9JHS2	Q9jhs2 rattus norv
26	76.5	50.0	859	2	Q6GQ12	Q6gq12 xenopus lae
27	74.5	48.7	835	2	Q696W2	Q696w2 ctenopharyn
28	74.5	48.7	862	2	Q6GL61	Q6gl61 xenopus tro
29	74.5	48.7	862	2	Q6GP97	Q6gp97 xenopus lae
30	74.5	48.7	873	2	Q8QGM4	Q8qgm4 fundulus he
31	74	48.4	632	2	Q96K34	Q96k34 homo sapien
32	70.5	46.1	163	2	Q6RYD1	Q6ryd1 sus scrofa
33	70.5	46.1	164	2	Q6RYD0	Q6ryd0 ovis aries
34	70.5	46.1	867	2	Q9W7C6	Q9w7c6 gallus gall
35	70.5	46.1	870	1	PAS1_HUMAN	Q99814 homo sapien
36	70.5	46.1	870	2	Q9XTA4	Q9xta4 bos taurus
37	70.5	46.1	870	2	Q9PTB3	Q9ptb3 coturnix co
38	70.5	46.1	874	1	PAS1_MOUSE	P97481 mus musculu
39	70.5	46.1	874	1	PAS1_RAT	Q9jhs1 rattus norv
40	70.5	46.1	874	2	Q6PEU2	Q6peu2 mus musculu
41	64.5	42.2	71	2	Q71939	Q71939 human immun
42	64.5	42.2	71	2	Q71945	Q71945 human immun
43	63.5	41.5	72	2	Q69628	Q69628 human immun
44	62.5	40.8	101	2	O71264	O71264 human immun
45	62	40.5	86	2	Q8ADC2	Q8adc2 human immun
46	61	39.9	72	2	P88699	P88699 human immun
47	60.5	39.5	101	2	Q6EK47	Q6ek47 human immun
48	60.5	39.5	101	2	Q72493	Q72493 human immun
49	59.5	38.9	101	2	Q6EG25	Q6eg25 human immun
50	59	38.6	86	2	Q8ADL8	Q8adl8 human immun
51	59	38.6	99	2	Q902T6	Q902t6 human immun
52	59	38.6	101	2	Q8Q7Z3	Q8q7z3 human immun
53	59	38.6	101	2	Q7ZJE0	Q7zje0 human immun
54	59	38.6	235	2	Q8QGI5	Q8qgi5 fundulus he
55	58.5	38.2	71	2	Q8AIK6	Q8aik6 human immun
56	58.5	38.2	71	2	Q8AIK7	Q8aik7 human immun
57	58.5	38.2	72	2	Q69627	Q69627 human immun
58	58.5	38.2	72	2	Q69632	Q69632 human immun
59	58.5	38.2	72	2	Q69635	Q69635 human immun
60	58.5	38.2	72	2	Q69637	Q69637 human immun
61	58.5	38.2	72	2	Q69638	Q69638 human immun
62	58.5	38.2	72	2	Q69639	Q69639 human immun
63	58.5	38.2	72	2	Q69641	Q69641 human immun
64	58.5	38.2	72	2	Q6GXZ1	Q6gxz1 human immun
65	58.5	38.2	72	2	Q70498	Q70498 human immun

ALIGNMENTS

RESULT 1
HIFA_ONCMY
ID HIFA_ONCMY STANDARD; PRT; 766 AA.
AC Q98SW2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN Name=HIF1A;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282949; PubMed=11278461; DOI=10.1074/jbc.M009057200;
RA Soitamo A.J., Rabergh C.M.I., Gassmann M., Sistonen L., Nikinmaa M.;
RT "Characterization of a hypoxia-inducible factor (HIF-1 alpha) from
RT rainbow trout: accumulation of protein occurs at normal venous oxygen
RT tension.";
RL J. Biol. Chem. 276:19699-19705(2001).
CC -!- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC gene promoters. Activation requires recruitment of transcriptional
CC coactivators (By similarity).
CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

```
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF304864; AAK30364.1; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; DNA-binding; Nuclear protein; Repeat;
KW   Transcription regulation.
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       82    159       PAS 1.
FT   DOMAIN      230    300       PAS 2.
FT   DOMAIN      304    347       PAC.
FT   DOMAIN      368    373       Poly-Glu.
SQ   SEQUENCE   766 AA;  85049 MW;  FC25A4984104DA5B CRC64;

  Query Match             64.1%;  Score 98;  DB 1;  Length 766;
  Best Local Similarity   82.6%;  Pred. No. 7.8e-05;
  Matches   19;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 QRRRDLDLEMLAXYIPMDDDFQL 30
              |   ||||||||:||||||||||
Db        547 QAMEDLDLEMLAPYIPMDDDFQL 569


RESULT 2
Q6EHI4
ID   Q6EHI4      PRELIMINARY;      PRT;   777 AA.
AC   Q6EHI4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypoxia inducible factor 1 alpha.
GN   Name=hif1a;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang C.-R., Tsai Y.-C., Young H.-W., Wang W.-D., Hu C.-H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY326951; AAQ91619.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   777 AA;  85897 MW;  A9AFE2D2732C7A33 CRC64;

  Query Match             63.4%;  Score 97;  DB 2;  Length 777;
  Best Local Similarity   82.6%;  Pred. No. 0.00011;
  Matches   19;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 QRRRDLDLEMLAXYIPMDDDFQL 30
              |   ||||||||:||||||||||
Db        545 QPMEDLDLEMLAPYIPMDDDFQL 567


RESULT 3
Q6STN7
ID   Q6STN7      PRELIMINARY;      PRT;   774 AA.
AC   Q6STN7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia-inducible factor-1alpha.
GN   Name=hif-1alpha;
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY450269; AAR95697.2; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   774 AA;  85741 MW;  15BD0B2F90C611C6 CRC64;

  Query Match             62.7%;  Score 96;  DB 2;  Length 774;
  Best Local Similarity   82.6%;  Pred. No. 0.00015;
  Matches   19;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 QRRRDLDLEMLAXYIPMDDDFQL 30
              |   ||||||||:||||||||||
Db        543 QAIEDLDLEMLAPYIPMDDDFQL 565


RESULT 4
Q6SLL1
ID   Q6SLL1      PRELIMINARY;      PRT;   786 AA.
AC   Q6SLL1;
```

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DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha subunit (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Spee B., Penning L.C., Rothuizen J.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY455802; AAR19225.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
FT   NON_TER       1       1
FT   NON_TER     786     786
SQ   SEQUENCE   786 AA;  88015 MW;  C37A27C25C343CDC CRC64;

  Query Match             62.1%;  Score 95;  DB 2;  Length 786;
  Best Local Similarity   94.7%;  Pred. No. 0.00021;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        536 DLDLEMLAPYIPMDDDFQL 554


RESULT 5
Q6PI54
ID   Q6PI54      PRELIMINARY;      PRT;   802 AA.
AC   Q6PI54;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hif1a-prov protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC043769; AAH43769.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   802 AA;  90177 MW;  30A571277A9A5B1F CRC64;

  Query Match             62.1%;  Score 95;  DB 2;  Length 802;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        550 DLDLEMLAPYIPMDDDFQL 568


RESULT 6
HIFA_XENLA
ID   HIFA_XENLA      STANDARD;      PRT;   805 AA.
AC   Q9I8A9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=HIF1A;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kietzmann T.;
RT   "Cloning and expression of the Xenopus laevis hypoxia inducible factor
RT   1 alpha homologue.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Binds to core DNA sequence 5'-
```

```
CC       [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC       gene promoters. Activation requires recruitment of transcriptional
CC       coactivators (By similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277829; CAB96628.1; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; FALSE_NEG.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; DNA-binding; Nuclear protein; Repeat;
KW   Transcription regulation.
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       85    157       PAS 1.
FT   DOMAIN      229    300       PAS 2.
FT   DOMAIN      303    346       PAC.
SQ   SEQUENCE   805 AA;  90964 MW;  BABFA0BD6B44FF3B CRC64;

  Query Match           62.1%;  Score 95;  DB 1;  Length 805;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        552 DLDLEMLAPYIPMDDDFQL 570


RESULT 7
HIFA_CHICK
ID   HIFA_CHICK     STANDARD;      PRT;   811 AA.
AC   Q9YIB9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=HIF1A;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Takahashi T.;
RT   "Molecular cloning and expression of an avian cDNA for hypoxia-
RT   inducible factor-1 alpha in embryonic ventricular myocytes.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC       [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC       gene promoters. Activation requires recruitment of transcriptional
CC       coactivators (By similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB013746; BAA34234.2; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; DNA-binding; Nuclear protein; Repeat;
KW   Transcription regulation.
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       80    157       PAS 1.
FT   DOMAIN      228    298       PAS 2.
FT   DOMAIN      302    345       PAC.
FT   DOMAIN      401    587       ODD.
FT   DOMAIN      529    573       NTAD.
FT   DOMAIN      576    785       ID.
FT   DOMAIN      703    706       Nuclear localization signal (Potential).
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DOMAIN      771    811       CTAD.
FT   DOMAIN      583    588       Poly-Ser.
SQ   SEQUENCE   811 AA;  90542 MW;  D14CD9FC98F064CB CRC64;

  Query Match           62.1%;  Score 95;  DB 1;  Length 811;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        554 DLDLEMLAPYIPMDDDFQL 572


RESULT 8
Q7YSE5
ID   Q7YSE5      PRELIMINARY;      PRT;   819 AA.
AC   Q7YSE5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia inducible factor 1 alpha subunit.
OS   Oryctolagus cuniculus (Rabbit).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clausen I., Kietz S., Fischer B.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY273790; AAP43517.1; -.
DR   HSSP; Q16665; 1H2K.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   819 AA;  91284 MW;  E11B4FBF7D4F6C7C CRC64;

  Query Match             62.1%;  Score 95;  DB 2;  Length 819;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 9
Q64F54
ID   Q64F54      PRELIMINARY;      PRT;   821 AA.
AC   Q64F54;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha subunit.
OS   Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Spermophilus.
OX   NCBI_TaxID=43179;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Morin P. Jr., Storey K.B.;
RT   "Cloning and expression of HIF-1 from the hibernating ground squirrel,
RT   Spermophilus tridecemlineatus.";
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY713478; AAU14021.1; -.
SQ   SEQUENCE   821 AA;  92028 MW;  4C96BD0355CCCE06 CRC64;

  Query Match             62.1%;  Score 95;  DB 2;  Length 821;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 10
HIFA_BOVIN
ID   HIFA_BOVIN     STANDARD;      PRT;   823 AA.
AC   Q9XTA5;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=HIF1A;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Artery;
RX   MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA   Hara S., Kobayashi C., Imura N.;
RT   "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-
RT   1alpha and -2alpha of bovine arterial endothelial cells.";
RL   Biochim. Biophys. Acta 1445:237-243(1999).
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Under hypoxic conditions activates
CC       the transcription of over 40 genes, including, erythropoietin,
CC       glucose transporters, glycolytic enzymes, vascular endothelial
CC       growth factor, and other genes whose protein products increase
CC       oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC       Plays an essential role in embryonic vascularization, tumor
CC       angiogenesis and pathophysiology of ischemic disease. Binds to
CC       core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC       element (HRE) of target gene promoters. Activation requires
CC       recruitment of transcriptional coactivators such as CREBPB and
CC       EP300. Activity is enhanced by interaction with both, NCOA1 or
CC       NCOA2. Interaction with redox regulatory protein APEX seems to
CC       activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC       CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-564 in the
CC       oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC       EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-564.
CC       The hydroxylated prolines promote interaction with VHL, initiating
CC       rapid ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-800 by HIF1AN, thus
CC       abrogating interaction with CREBBP and EP300 and preventing
CC       transcriptional activation (By similarity).
CC   -!- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC       nitrosylation in vitro, however not all thiol groups seem to be
CC       nitrolysated in vivo (By similarity).
CC   -!- PTM: Acetylation of Lys-532 by ARD1 increases interaction with VHL
CC       and stimulates subsequent proteasomal degradation (By similarity).
CC   -!- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB018398; BAA78675.1; -.
DR   HSSP; Q16665; 1L8C.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
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DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
KW   Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       85    158       PAS 1.
FT   DOMAIN      228    298       PAS 2.
FT   DOMAIN      302    345       PAC.
FT   DOMAIN      401    600       ODD.
FT   DOMAIN      531    575       NTAD.
FT   DOMAIN      576    782       ID.
FT   DOMAIN      783    823       CTAD.
FT   DOMAIN      715    718       Nuclear localization signal (Potential).
FT   MOD_RES      90     90       S-nitrosocysteine (Potential).
FT   MOD_RES     139    139       S-nitrosocysteine (Potential).
FT   MOD_RES     173    173       S-nitrosocysteine (Potential).
FT   MOD_RES     194    194       S-nitrosocysteine (Potential).
FT   MOD_RES     210    210       S-nitrosocysteine (Potential).
FT   MOD_RES     219    219       S-nitrosocysteine (Potential).
FT   MOD_RES     224    224       S-nitrosocysteine (Potential).
FT   MOD_RES     255    255       S-nitrosocysteine (Potential).
FT   MOD_RES     334    334       S-nitrosocysteine (Potential).
FT   MOD_RES     337    337       S-nitrosocysteine (Potential).
FT   MOD_RES     359    359       S-nitrosocysteine (Potential).
FT   MOD_RES     402    402       Hydroxyproline (By similarity).
FT   MOD_RES     520    520       S-nitrosocysteine (Potential).
FT   MOD_RES     532    532       N6-acetyllysine (By similarity).
FT   MOD_RES     564    564       Hydroxyproline (By similarity).
FT   MOD_RES     755    755       S-nitrosocysteine (Potential).
FT   MOD_RES     777    777       S-nitrosocysteine (Potential).
FT   MOD_RES     797    797       S-nitrosocysteine (Potential).
FT   MOD_RES     800    800       3-hydroxyasparagine (By similarity).
SQ   SEQUENCE   823 AA;  92127 MW;  12674E467A61B1A1 CRC64;

  Query Match             62.1%;  Score 95;  DB 1;  Length 823;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 11
Q6IV47
ID   Q6IV47      PRELIMINARY;      PRT;   823 AA.
AC   Q6IV47;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia inducible factor-1a.
GN   Name=HIF-1A;
OS   Bos mutus grunniens (Yak).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=30521;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dolt K.S., Qadar Pasha M.A.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY621118; AAT39520.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   823 AA;  92128 MW;  A6E388E4PEA15705 CRC64;

  Query Match             62.1%;  Score 95;  DB 2;  Length 823;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 12
Q6H8T3
ID   Q6H8T3      PRELIMINARY;      PRT;   824 AA.
AC   Q6H8T3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia inducible factor 1 alpha.
GN   Name=hif-1a;
OS   Spalax judaei (Blind subterranean mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC   Spalax.
OX   NCBI_TaxID=134510;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Shams I., Avivi A., Nevo E.;
RT   "Hypoxic stress tolerance of the subterranean mole rat: Expression of
RT   erythropoietin and hypoxia-inducible factor-1a.";
RL   Nucleic Acids Res. 0:0-0(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=15210955; DOI=10.1073/pnas.0403540101;
RA   Shams I., Avivi A., Eviatar N.;
RT   "Hypoxic stress tolerance of the blind subterranean mole rat:
RT   expression of erythropoietin and hypoxia-inducible factor 1 alpha.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9698-9703(2004).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AJ715791; CAG29396.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
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DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   824 AA;  92161 MW;  33A1DDC3593CBFFF CRC64;

  Query Match           62.1%;  Score 95;  DB 2;  Length 824;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              ||||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 13
HIFA_RAT
ID   HIFA_RAT       STANDARD;      PRT;   825 AA.
AC   O35800; Q9WTU9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN   Name=Hif1a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Hepatocytes;
RX   MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA   Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;
RT   "Perivenous expression of the mRNA of the three hypoxia-inducible
RT   factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL   Biochem. J. 354:531-537(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX   MEDLINE=21417706; PubMed=11526200;
RA   Zou A.-P., Yang Z.-Z., Li P.-L., Cowley A.W. Jr.;
RT   "Oxygen-dependent expression of hypoxia-inducible factor-1alpha in
RT   renal medullary cells of rats.";
RL   Physiol. Genomics 6:159-168(2001).
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Under hypoxic conditions activates
CC       the transcription of over 40 genes, including, erythropoietin,
CC       glucose transporters, glycolytic enzymes, vascular endothelial
CC       growth factor, and other genes whose protein products increase
CC       oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC       Plays an essential role in embryonic vascularization, tumor
CC       angiogenesis and pathophysiology of ischemic disease. Binds to
CC       core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC       element (HRE) of target gene promoters. Activation requires
CC       recruitment of transcriptional coactivators such as CREBPB and
CC       EP300. Activity is enhanced by interaction with both, NCOA1 or
CC       NCOA2. Interaction with redox regulatory protein APEX seems to
CC       activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC       CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in the kidney, higher expression is
CC       seen in the renal medulla than in the cortex. Expressed also in
CC       the perivenous zone of the liver.
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-563 in the
CC       oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC       EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-563.
CC       The hydroxylated prolines promote interaction with VHL, initiating
CC       rapid ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-802 by HIF1AN, thus
CC       abrogating interaction with CREBBP and EP300 and preventing
CC       transcriptional activation (By similarity).
CC   -!- PTM: S-nitrosylated. All free thiol groups are subjected to S-
CC       nitrosylation in vitro, however not all thiol groups seem to be
CC       nitrolysated in vivo (By similarity).
CC   -!- PTM: Acetylation of Lys-531 by ARD1 increases interaction with VHL
CC       and stimulates subsequent proteasomal degradation (By similarity).
CC   -!- PTM: Phosphorylation is required for DNA binding (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y09507; CAA70701.1; -.
DR   EMBL; AF057308; AAD24413.1; -.
DR   HSSP; Q16665; 1L8C.
DR   TRANSFAC; T05461; -.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001321; HypoxindF1A.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR01080; HYPOXIAIF1A.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   Acetylation; Activator; DNA-binding; Hydroxylation; Nuclear protein;
KW   Phosphorylation; Repeat; S-nitrosylation; Transcription regulation.
FT   DOMAIN      718    721       Nuclear localization signal (Potential).
FT   DNA_BIND     17     30       Basic motif.
FT   DOMAIN       31     71       Helix-loop-helix motif.
FT   DOMAIN       85    158       PAS 1.
FT   DOMAIN      228    298       PAS 2.
FT   DOMAIN      302    345       PAC.
FT   DOMAIN      401    602       ODD.
FT   DOMAIN      530    574       NTAD.
FT   DOMAIN      575    784       ID.
FT   DOMAIN      717    720       Nuclear localization signal (Potential).
FT   DOMAIN      785    825       CTAD.
FT   MOD_RES      90     90       S-nitrosocysteine (Potential).
FT   MOD_RES     139    139       S-nitrosocysteine (Potential).
FT   MOD_RES     173    173       S-nitrosocysteine (Potential).
FT   MOD_RES     194    194       S-nitrosocysteine (Potential).
FT   MOD_RES     210    210       S-nitrosocysteine (Potential).
FT   MOD_RES     219    219       S-nitrosocysteine (Potential).
FT   MOD_RES     224    224       S-nitrosocysteine (Potential).
FT   MOD_RES     255    255       S-nitrosocysteine (Potential).
FT   MOD_RES     334    334       S-nitrosocysteine (Potential).
FT   MOD_RES     337    337       S-nitrosocysteine (Potential).
FT   MOD_RES     385    385       S-nitrosocysteine (Potential).
FT   MOD_RES     402    402       Hydroxyproline (By similarity).
FT   MOD_RES     519    519       S-nitrosocysteine (Potential).
FT   MOD_RES     531    531       N6-acetyllysine (By similarity).
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FT   MOD_RES     563    563       Hydroxyproline (By similarity).
FT   MOD_RES     779    779       S-nitrosocysteine (Potential).
FT   MOD_RES     799    799       S-nitrosocysteine (Potential).
FT   MOD_RES     802    802       3-hydroxyasparagine (By similarity).
FT   CONFLICT     12     12       K -> NR (in Ref. 2).
FT   CONFLICT     74     74       D -> G (in Ref. 2).
FT   CONFLICT     96     96       P -> L (in Ref. 2).
FT   CONFLICT    329    329       D -> N (in Ref. 2).
FT   CONFLICT    613    619       ATATTAT -> TATA (in Ref. 2).
FT   CONFLICT    708    708       R -> K (in Ref. 2).
SQ   SEQUENCE   825 AA;  92319 MW;  C4109A57F38667E9 CRC64;

  Query Match             62.1%;  Score 95;  DB 1;  Length 825;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 DLDLEMLAXYIPMDDDFQL 30
               |||||||||:|||||||||||
Db         555 DLDLEMLAPYIPMDDDFQL 573


RESULT 14
HIFA_HUMAN
ID   HIFA_HUMAN     STANDARD;      PRT;   826 AA.
AC   Q16665; Q96PT9; Q9UPB1;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE   interacting protein) (Member of PAS protein 1) (MOP1).
GN   Name=HIF1A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
RX   MEDLINE=95296340; PubMed=7539918;
RA   Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;
RT   "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
RT   heterodimer regulated by cellular O2 tension.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hepatoma;
RX   MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA   Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA   Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT   "Characterization of a subset of the basic-helix-loop-helix-PAS
RT   superfamily that interacts with components of the dioxin signaling
RT   pathway.";
RL   J. Biol. Chem. 272:8581-8593(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99000835; PubMed=9782081; DOI=10.1006/geno.1998.5416;
RA   Iyer N.V., Leung S.W., Semenza G.L.;
RT   "The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
RT   evolutionary conservation.";
RL   Genomics 52:159-165(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Rupert J.L., Hochachka P.W.;
RT   "HIF1a sequence in the Quechua, a high altitude population.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Glial tumor;
RA   Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Liver;
RA   Tanaka S., Sugimachi K.;
RT   "Hypoxia-inducible factor-1 alpha variant isolated from human liver
RT   tissue.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Choriocarcinoma, and Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   TRANSACTIVATION DOMAINS NTAD AND CTAD.
RX   MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;
RA   Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;
RT   "Transactivation and inhibitory domains of hypoxia-inducible factor
RT   1alpha. Modulation of transcriptional activity by oxygen tension.";
RL   J. Biol. Chem. 272:19253-19260(1997).
RN   [9]
RP   SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.
RX   MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;
RA   Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,
RA   Poellinger L.;
RT   "Signal transduction in hypoxic cells: inducible nuclear translocation
RT   and recruitment of the CBP/p300 coactivator by the hypoxia-inducible
RT   factor-1alpha.";
RL   EMBO J. 17:6573-6586(1998).
RN   [10]
RP   OXYGEN-DEPENDENT DEGRADATION DOMAIN.
RX   MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;
RA   Huang L.E., Gu J., Schau M., Bunn H.F.;
RT   "Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-
RT   dependent degradation domain via the ubiquitin-proteasome pathway.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992(1998).
RN   [11]
RP   TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP   MUTAGENESIS OF CYS-800.
RX   MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA   Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA   Poellinger L., Fujii-Kuriyama Y.;
RT   "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT   in response to hypoxia: their stabilization and redox signal-induced
RT   interaction with CBP/p300.";
RL   EMBO J. 18:1905-1914(1999).
RN   [12]
RP   INTERACTION WITH NCOA1; NCOA2 AND APEX.
RX   MEDLINE=20063199; PubMed=10594042;
RA   Carrero P., Okamoto K., Coumailleau P., O'Brien S., Tanaka H.,
RA   Poellinger L.;
RT   "Redox-regulated recruitment of the transcriptional coactivators CREB-
RT   binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";
RL   Mol. Cell. Biol. 20:402-415(2000).
RN   [13]
RP   MUTAGENESIS OF SER-551 AND THR-552.
RX   MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;
RA   Sutter C.H., Laughner E., Semenza G.L.;
RT   "Hypoxia-inducible factor 1alpha protein expression is controlled by
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RT   oxygen-regulated ubiquitination that is disrupted by deletions and
RT   missense mutations.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753(2000).
RN   [14]
RP   UBIQUITINATION.
RX   MEDLINE=21214630; PubMed=11292861; DOI=10.1126/science.1059796;
RA   Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
RA   Gaskell S.J., von Kriegsheim A., Hebestreit H.F., Mukherji M.,
RA   Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.;
RT   "Targeting of HIF-alpha to the von Hippel-Lindau ubiquitylation
RT   complex by O2-regulated prolyl hydroxylation.";
RL   Science 292:468-472(2001).
RN   [15]
RP   S-NITROSYLATION.
RX   MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793(02)03887-5;
RA   Sumbayev V.V., Budde A., Zhou J., Bruene B.;
RT   "HIF-1 alpha protein as a target for S-nitrosation.";
RL   FEBS Lett. 535:106-112(2003).
RN   [16]
RP   ACETYLATION OF LYS-532.
RX   MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674(02)01085-1;
RA   Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
RA   Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
RT   "Regulation and destabilization of HIF-1alpha by ARD1-mediated
RT   acetylation.";
RL   Cell 111:709-720(2002).
RN   [17]
RP   HYDROXYLATION OF ASN-803.
RX   MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA   Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA   Bruick R.K.;
RT   "FIH-1 is an asparaginyl hydroxylase enzyme that regulates the
RT   transcriptional activity of hypoxia-inducible factor.";
RL   Genes Dev. 16:1466-1471(2002).
RN   [18]
RP   HYDROXYLATION OF PRO-402 AND PRO-564.
RX   MEDLINE=21558830; PubMed=11598268; DOI=10.1126/science.1066373;
RA   Bruick R.K., McKnight S.L.;
RT   "A conserved family of prolyl-4-hydroxylases that modify HIF.";
RL   Science 294:1337-1340(2001).
RN   [19]
RP   REVIEW.
RX   MEDLINE=20407247; PubMed=10950862;
RA   Semenza G.L.;
RT   "HIF-1 and human disease: one highly involved factor.";
RL   Genes Dev. 14:1983-1991(2000).
RN   [20]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=20539371; PubMed=11089639;
RA   Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
RA   Michiels C.;
RT   "A model for the complex between the hypoxia-inducible factor-1 (HIF-
RT   1) and its consensus DNA sequence.";
RL   J. Biomol. Struct. Dyn. 18:169-179(2000).
RN   [21]
RP   X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
RP   HIF1AN.
RX   MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
RA   Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.F.,
RA   Schlemminger I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
RT   "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
RT   mechanism of oxidative modification of HIF-1 alpha.";
RL   J. Biol. Chem. 278:1802-1806(2003).
RN   [22]
RP   STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
RX   MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
RA   Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
RA   Wagner G., Eck M.J.;
RT   "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
RT   factor-1 alpha.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372(2002).
RN   [23]
RP   STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.
RX   MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
RA   Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
RA   Wright P.E.;
RT   "Structural basis for Hif-1 alpha /CBP recognition in the cellular

  Query Match             62.1%;  Score 95;  DB 1;  Length 826;
  Best Local Similarity   94.7%;  Pred. No. 0.00022;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              |||||||:||||||||||
Db        556 DLDLEMLAPYIPMDDDFQL 574


RESULT 15
HIFA_MOUSE
ID   HIFA_MOUSE     STANDARD;      PRT;   836 AA.
AC   Q61221; O08741; O08993; Q61664; Q61665; Q8C681; Q8CC19; Q8CCB6;
AC   Q8R385; Q9CYA8;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE   interacting protein).
GN   Name=Hif1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   STRAIN=C57BL/6; TISSUE=Hepatocytes;
RX   MEDLINE=96355491; PubMed=8702901; DOI=10.1074/jbc.271.35.21262;
RA   Li H., Ko H.P., Whitlock J.P. Jr.;
RT   "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
RT   Roles of Arnt and HIF1alpha.";
RL   J. Biol. Chem. 271:21262-21267(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=129/SvJ;
RX   MEDLINE=98034461; PubMed=9368100;
RA   Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
RA   Bradfield C.A.;
RT   "Molecular characterization of the murine Hif-1 alpha locus.";
RL   Gene Expr. 6:287-299(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   STRAIN=129/Sv;
RX   MEDLINE=97354184; PubMed=9210478;
RA   Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
RA   Gassmann M.;
RT   "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
RT   organization, expression and characterization of an alternative first
RT   exon and 5' flanking sequence.";
RL   Eur. J. Biochem. 246:155-165(1997).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C57BL/6J; TISSUE=Colon, Diencephalon, Embryo, and Skin;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 13-822 FROM N.A. (ISOFORM 2).
RC   TISSUE=Hepatocytes;
RX   MEDLINE=96254028; PubMed=8660378; DOI=10.1006/bbrc.1996.0845;
RA   Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.;
RT   "Nucleotide sequence, chromosomal assignment and mRNA expression of
RT   mouse hypoxia-inducible factor-1 alpha.";
RL   Biochem. Biophys. Res. Commun. 223:54-59(1996).
RN   [7]
RP   SEQUENCE OF 22-85 FROM N.A.
RC   TISSUE=Hepatocytes;
RA   O'Rourke J.F.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Functions as a master transcriptional regulator of the
CC       adaptive response to hypoxia. Under hypoxic conditions activates
CC       the transcription of over 40 genes, including, erythropoietin,
CC       glucose transporters, glycolytic enzymes, vascular endothelial
CC       growth factor, and other genes whose protein products increase
CC       oxygen delivery or facilitate metabolic adaptation to hypoxia.
CC       Plays an essential role in embryonic vascularization, tumor
CC       angiogenesis and pathophysiology of ischemic disease. Binds to
CC       core DNA sequence 5'-[AG]CGTG-3' within the hypoxia response
CC       element (HRE) of target gene promoters. Activation requires
CC       recruitment of transcriptional coactivators such as CREBPB and
CC       EP300. Activity is enhanced by interaction with both, NCOA1 or
CC       NCOA2. Interaction with redox regulatory protein APEX seems to
CC       activate CTAD and potentiates activation by NCOA1 and CREBBP (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC       alpha and a beta/ARNT subunit. Binds to the TAZ-type 1 domains of
CC       CREBBP and EP300. Interacts with NCOA1, NCOA2, APEX and HSP90 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC       translocation in response to hypoxia (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q61221-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q61221-2; Sequence=VSP_007739;
CC   -!- TISSUE SPECIFICITY: Ubiquitous.
CC   -!- DOMAIN: Contains two independent C-terminal transactivation
CC       domains, NTAD and CTAD, which function synergistically. Their
CC       transcriptional activity is repressed by an intervening inhibitory
CC       domain (ID) (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Pro-402 and Pro-577 in the
CC       oxygen-dependent degradation domain (ODD) by EGLN1/PHD1 and
CC       EGLN2/PHD2. EGLN3/PHD3 has also been shown to hydroxylate Pro-577.
CC       The hydroxylated prolines promote interaction with VHL, initiating
CC       rapid ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-813 by HIF1AN, thus
CC       abrogating interaction with CREBBP and EP300 and preventing
CC       transcriptional activation (By similarity).
CC   -!- PTM: S-nitrosylated. All 15 free thiol groups are subjected to S-
CC       nitrosylation in vitro, however not all thiol groups seem to be
CC       nitrolysated in vivo (By similarity).
CC   -!- PTM: Acetylation of Lys-545 by ARD1 increases interaction with VHL
CC       and stimulates subsequent proteasomal degradation (By similarity).
CC   -!- PTM: Requires phosphorylation for DNA-binding (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U59496; AAC52730.1; -.
DR   EMBL; AF003695; AAC53455.1; -.
DR   EMBL; Y09085; CAA70306.1; -.
DR   EMBL; Y13656; CAA70306.1; JOINED.
DR   EMBL; Y09085; CAA70305.1; -.
DR   EMBL; AF004155; AAC53461.1; -.
DR   EMBL; AF004141; AAC53461.1; JOINED.
DR   EMBL; AF004142; AAC53461.1; JOINED.
DR   EMBL; AF004143; AAC53461.1; JOINED.
DR   EMBL; AF004144; AAC53461.1; JOINED.
DR   EMBL; AF004145; AAC53461.1; JOINED.
DR   EMBL; AF004146; AAC53461.1; JOINED.
DR   EMBL; AF004147; AAC53461.1; JOINED.
DR   EMBL; AF004148; AAC53461.1; JOINED.
DR   EMBL; AF004149; AAC53461.1; JOINED.
DR   EMBL; AF004150; AAC53461.1; JOINED.
DR   EMBL; AF004151; AAC53461.1; JOINED.
DR   EMBL; AF004152; AAC53461.1; JOINED.
DR   EMBL; AF004153; AAC53461.1; JOINED.
DR   EMBL; AF004154; AAC53461.1; JOINED.
DR   EMBL; AK034087; BAC28578.1; -.
DR   EMBL; AK076395; BAC36320.1; -.
DR   EMBL; AK033471; BAC28305.1; -.
DR   EMBL; AK017853; BAB30975.1; -.
DR   EMBL; BC026139; AAH26139.1; -.
DR   EMBL; X95580; CAA64833.1; -.
DR   EMBL; X95002; CAA64458.1; -.
DR   PIR; JC4837; JC4837.
DR   TRANSFAC; T04666; -.
DR   MGD; MGI:106918; Hif1a.
DR   GO; GO:0009434; C:flagellum (sensu Eukarya); IDA.

  Query Match           62.1%;  Score 95;  DB 1;  Length 836;
  Best Local Similarity 94.7%;  Pred. No. 0.00023;
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  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
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Db        569 DLDLEMLAPYIPMDDDFQL 587


RESULT 16
Q9QX54
ID   Q9QX54      PRELIMINARY;      PRT;   630 AA.
AC   Q9QX54;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia-inducible factor 3 alpha (Fragment).
GN   Name=Hif3a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gu Y.-Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT   "Cloning and Characterization of a Third Hypoxia Inducible Factor,
RT   HIF3-alpha.";
RL   J. Biol. Chem. 0:0-0(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99054547; PubMed=9840812;
RA   Gu Y.Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT   "Molecular characterization and chromosomal localization of a third
RT   alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL   Gene Expr. 7:205-213(1998).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF079153; AAF21782.1; -.
DR   EMBL; AF079140; AAF21782.1; JOINED.
DR   EMBL; AF079141; AAF21782.1; JOINED.
DR   EMBL; AF079143; AAF21782.1; JOINED.
DR   EMBL; AF079145; AAF21782.1; JOINED.
DR   EMBL; AF079147; AAF21782.1; JOINED.
DR   EMBL; AF079149; AAF21782.1; JOINED.
DR   EMBL; AF079151; AAF21782.1; JOINED.
DR   EMBL; AF079152; AAF21782.1; JOINED.
DR   EMBL; AF079150; AAF21782.1; JOINED.
DR   EMBL; AF079148; AAF21782.1; JOINED.
DR   EMBL; AF079146; AAF21782.1; JOINED.
DR   EMBL; AF079144; AAF21782.1; JOINED.
DR   EMBL; AF079142; AAF21782.1; JOINED.
DR   HSSP; Q99814; 1P97.
DR   MGD; MGI:1859778; Hif3a.
DR   GO; GO:0005634; C:nucleus; IC.
DR   GO; GO:0003700; F:transcription factor activity; IPI.
DR   GO; GO:0001666; P:response to hypoxia; IDA.
DR   GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
FT   NON_TER     630    630
SQ   SEQUENCE   630 AA;  69623 MW;  828EB2CB4E6D45B6 CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 630;
  Best Local Similarity   88.9%;  Pred. No. 0.015;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        480 LDLEMLAPYISMDDDFQL 497


RESULT 17
Q8WXA1
ID   Q8WXA1      PRELIMINARY;      PRT;   632 AA.
AC   Q8WXA1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Inhibitory PAS domain protein.
GN   Name=IPAS;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheng J.Q.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF463492; AAL69947.1; -.
DR   HSSP; Q16665; 1LQB.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   632 AA;  68963 MW;  9665B0AF3998F8EF CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 632;
  Best Local Similarity   88.9%;  Pred. No. 0.015;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        485 LDLEMLAPYISMDDDFQL 502


RESULT 18
Q6STN6
ID   Q6STN6      PRELIMINARY;      PRT;   643 AA.
AC   Q6STN6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypoxia-inducible factor-4alpha.
GN   Name=hif-4alpha;
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Law S.H.W., Wu R.S.S., Mok H.O.L., Yu R.M.K., Ng P.K.S., Kong R.Y.C.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY450270; AAR95698.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
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DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   643 AA;  72434 MW;  D73C6DDD10086C4D CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 643;
  Best Local Similarity   59.3%;  Pred. No. 0.015;
  Matches   16;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 KKRRQRRRDLDLEMLAXYIPMDDDFQL 30
              | : :   :|||:|||:|| |||||||
Db        487 KGQSEAMDELDLDMLAPYISMDDDFQL 513


RESULT 19
Q9HAI2
ID   Q9HAI2      PRELIMINARY;      PRT;   648 AA.
AC   Q9HAI2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ11591.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole embryo;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
DR   EMBL; AK021653; BAB13865.1; -.
DR   HSSP; Q16665; 1LQB.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00989; PAS; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   648 AA;  69995 MW;  EBEFC744BC3F148E CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 648;
  Best Local Similarity   88.9%;  Pred. No. 0.015;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        429 LDLEMLAPYISMDDDFQL 446


RESULT 20
Q9Z2I5
ID   Q9Z2I5      PRELIMINARY;      PRT;   662 AA.
AC   Q9Z2I5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia inducible factor three alpha.
GN   Name=Hif3a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99054547; PubMed=9840812;
RA   Gu Y.Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield C.A.;
RT   "Molecular characterization and chromosomal localization of a third
RT   alpha-class hypoxia inducible factor subunit, HIF3alpha.";
RL   Gene Expr. 7:205-213(1998).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF060194; AAC72734.1; -.
DR   HSSP; Q99814; 1P97.
DR   MGD; MGI:1859778; Hif3a.
DR   GO; GO:0005634; C:nucleus; IC.
DR   GO; GO:0003700; F:transcription factor activity; IPI.
DR   GO; GO:0001666; P:response to hypoxia; IDA.
DR   GO; GO:0006366; P:transcription from Pol II promoter; IPI.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   662 AA;  73012 MW;  58740A1B6993D3B5 CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 662;
  Best Local Similarity   88.9%;  Pred. No. 0.016;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        480 LDLEMLAPYISMDDDFQL 497


RESULT 21
Q9Y2N7
ID   Q9Y2N7      PRELIMINARY;      PRT;   667 AA.
AC   Q9Y2N7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative homolog of hypoxia inducible factor three alpha (Hypoxia-
DE   inducible factor-3 alpha).
GN   Name=HIF-3A;
```

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA   Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.;
RA   Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA   Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA   Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA   Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA   Olsen A.S., Carrano A.V.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=21458277; PubMed=11573933; DOI=10.1006/bbrc.2001.5659;
RA   Hara S., Hamada J., Kobayashi C., Kondo Y., Imura N.;
RT   "Expression and characterization of hypoxia-inducible factor (HIF)-
RT   3alpha in human kidney: suppression of HIF-mediated gene expression by
RT   HIF-3alpha.";
RL   Biochem. Biophys. Res. Commun. 287:808-813(2001).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AC007193; AAD22668.1; -.
DR   EMBL; AB054067; BAB69689.1; -.
DR   PIR; JC7771; JC7771.
DR   HSSP; Q16665; 1LQB.
DR   Genew; HGNC:15825; HIF3A.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   667 AA;  72404 MW;  67B8794FF9DCCF4B CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 667;
  Best Local Similarity   88.9%;  Pred. No. 0.016;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        483 LDLEMLAPYISMDDDFQL 500


RESULT 22
Q66K72
ID   Q66K72      PRELIMINARY;      PRT;   669 AA.
AC   Q66K72;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   HIF3A protein.
GN   Name=HIF3A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC080551; AAH80551.1; -.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   669 AA;  72460 MW;  7EF7362A1691AE6D CRC64;

  Query Match             52.9%;  Score 81;  DB 2;  Length 669;
  Best Local Similarity   88.9%;  Pred. No. 0.016;
  Matches   16;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| |||||||
Db        485 LDLEMLAPYISMDDDFQL 502


RESULT 23
Q7T2E4
ID   Q7T2E4      PRELIMINARY;      PRT;   571 AA.
AC   Q7T2E4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein hif1al.
GN   Name=hif1al;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054582; AAH54582.1; -.
DR   HSSP; Q99814; 1P97.
DR   ZFIN; ZDB-GENE-040426-1315; hif1al.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   571 AA;  63846 MW;  1BA8E4CC29F16672 CRC64;

  Query Match             52.3%;  Score 80;  DB 2;  Length 571;
  Best Local Similarity   78.9%;  Pred. No. 0.018;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              :|||:|||:|| |||||||
Db        430 ELDLDMLAPYISMDDDFQL 448


RESULT 24
Q6EGR9
ID   Q6EGR9      PRELIMINARY;      PRT;   626 AA.
AC   Q6EGR9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hif3a.
GN   Name=hif3a;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang C.-R., Hu C.-H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY330295; AAQ94179.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   626 AA;  70221 MW;  EA12390DFECF90B9 CRC64;

  Query Match             52.3%;  Score 80;  DB 2;  Length 626;
  Best Local Similarity   78.9%;  Pred. No. 0.02;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 DLDLEMLAXYIPMDDDFQL 30
              :|||:|||:|| |||||||
Db        485 ELDLDMLAPYISMDDDFQL 503


RESULT 25
Q9JHS2
ID   Q9JHS2      PRELIMINARY;      PRT;   662 AA.
AC   Q9JHS2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia inducible factor 3 alpha.
GN   Name=Hif-3a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA   Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;
RT   "Perivenous expression of the mRNA of the three hypoxia-inducible
RT   factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL   Biochem. J. 354:531-537(2001).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AJ277827; CAB96611.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   662 AA;  72887 MW;  AC9672E340544010 CRC64;

  Query Match             51.3%;  Score 78.5;  DB 2;  Length 662;
  Best Local Similarity   50.0%;  Pred. No. 0.035;
  Matches   18;  Conservative    3;  Mismatches    6;  Indels    9;  Gaps    1;

Qy          4 KKRRQRRRDL---------DLEMLAXYIPMDDDFQL 30
              :| :    ||         ||||||:|| |||||||
Db        462 RKNKTMETDLDIAQDPDTPDLEMLAPYISMDDDFQL 497


RESULT 26
Q6GQ12
ID   Q6GQ12      PRELIMINARY;      PRT;   859 AA.
AC   Q6GQ12;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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```
DE   MGC80468 protein.
GN   Name=MGC80468;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC072936; AAH72936.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   859 AA;  96956 MW;  59D477E1929A0AD6 CRC64;

  Query Match            50.0%;  Score 76.5;  DB 2;  Length 859;
  Best Local Similarity  76.2%;  Pred. No. 0.087;
  Matches   16;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         11 RDLDLEMLAXYIPMD-DDFQL 30
              :||||| ||:||||| :||||
Db        516 KDLDLETLAPYIPMDGEDFQL 536
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RESULT 27
Q696W2
ID   Q696W2      PRELIMINARY;      PRT;   835 AA.
AC   Q696W2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypoxia-inducible factor 2 alpha.
GN   Name=hif-2alpha;
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Law S.H.W., Kong R.Y.C., Wu R.S.S.;
RT   "Molecular characterization of hypoxia-inducible factor-2alpha (hif-
RT   2alpha) gene in grass carp.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AY577524; AAT76668.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   835 AA;  92830 MW;  CAE59E9AAFC785FD CRC64;

  Query Match            48.7%;  Score 74.5;  DB 2;  Length 835;
  Best Local Similarity  80.0%;  Pred. No. 0.16;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              ||||| ||:||||| :||||
Db        518 DLDLETLAPYIPMDGEDFQL 537


RESULT 28
Q6GL61
ID   Q6GL61      PRELIMINARY;      PRT;   862 AA.
AC   Q6GL61;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Epas1-prov protein.
GN   Name=epas1-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC074648; AAH74648.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   862 AA;  97138 MW;  C2976D62101531CE CRC64;

  Query Match            48.7%;  Score 74.5;  DB 2;  Length 862;
  Best Local Similarity   80.0%;  Pred. No. 0.17;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              ||||| ||:||||| :||||
Db        517 DLDLETLAPYIPMDGEDFQL 536


RESULT 29
Q6GP97
ID   Q6GP97      PRELIMINARY;      PRT;   862 AA.
AC   Q6GP97;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80589 protein.
GN   Name=MGC80589;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC073244; AAH73244.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   862 AA;  97319 MW;  3AC8FB39032E9E60 CRC64;

  Query Match            48.7%;  Score 74.5;  DB 2;  Length 862;
  Best Local Similarity   80.0%;  Pred. No. 0.17;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              ||||| ||:||||| :||||
Db        518 DLDLETLAPYIPMDGEDFQL 537


RESULT 30
Q8QGM4
ID   Q8QGM4      PRELIMINARY;      PRT;   873 AA.
AC   Q8QGM4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia-inducible factor 2 alpha.
OS   Fundulus heteroclitus (Killifish) (Mummichog).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Cyprinodontiformes; Fundulidae; Fundulus.
OX   NCBI_TaxID=8078;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21929980; PubMed=11932946; DOI=10.1002/jez.10074;
RA   Powell W.H., Hahn M.E.;
RT   "Identification and functional characterization of Hypoxia-inducible
RT   factor 2alpha from the estuaring teleost, Fundulus heteroclitus:
RT   Interaction of HIF2a with two ARNT2 splice variants.";
RL   J. Exp. Zool. 294:17-29(2002).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF402782; AAL95711.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   873 AA;  96437 MW;  BA2CF40AB4ABC7B0 CRC64;

  Query Match           48.7%;  Score 74.5;  DB 2;  Length 873;
  Best Local Similarity  80.0%;  Pred. No. 0.17;
  Matches   16;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              ||||| ||:||||| :||||
Db        541 DLDLETLAPYIPMDGEDFQL 560


RESULT 31
Q96K34
ID   Q96K34      PRELIMINARY;      PRT;   632 AA.
AC   Q96K34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ14819.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AK027725; BAB55324.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   632 AA;  68933 MW;  A19F1ED3D05E7A71 CRC64;

  Query Match           48.4%;  Score 74;  DB 2;  Length 632;
  Best Local Similarity  83.3%;  Pred. No. 0.14;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 LDLEMLAXYIPMDDDFQL 30
              |||||||:|| | |||||
Db        485 LDLEMLAPYISMGDDFQL 502


RESULT 32
Q6RYD1
ID   Q6RYD1      PRELIMINARY;      PRT;   163 AA.
AC   Q6RYD1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Endothelial PAS domain protein 1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ing N.H., Balog C.J., Wolfskill R.L.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY485673; AAR37390.1; -.
FT   NON_TER       1      1
FT   NON_TER     163    163
SQ   SEQUENCE   163 AA;  17207 MW;  679CDA9F183CCAD3 CRC64;

  Query Match           46.1%;  Score 70.5;  DB 2;  Length 163;
```

```
  Best Local Similarity   75.0%;  Pred. No. 0.098;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        118 ELDLETLAPYIPMDGEDFQL 137


RESULT 33
Q6RYD0
ID   Q6RYD0      PRELIMINARY;      PRT;   164 AA.
AC   Q6RYD0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Endothelial PAS domain protein 1 (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ing N.H., Balog C.J., Wolfskill R.L.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY485674; AAR37391.1; -.
FT   NON_TER       1      1
FT   NON_TER     164    164
SQ   SEQUENCE   164 AA;  17405 MW;  49DBB95BA3D6D826 CRC64;

  Query Match             46.1%;  Score 70.5;  DB 2;  Length 164;
  Best Local Similarity   75.0%;  Pred. No. 0.099;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        119 ELDLETLAPYIPMDGEDFQL 138


RESULT 34
Q9W7C6
ID   Q9W7C6      PRELIMINARY;      PRT;   867 AA.
AC   Q9W7C6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Endothelial PAS domain protein 1.
GN   Name=EPAS1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=breed White Leghorn;
RX   MEDLINE=20047819; PubMed=10580084; DOI=10.1016/S0014-5793(99)01476-3;
RA   Favier J., Kempf H., Corvol P., Gasc J.-M.;
RT   "Cloning and expression pattern of EPAS1 in the chicken embryo.
RT   Colocalization with tyrosine hydroxylase.";
RL   FEBS Lett. 462:19-24(1999).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF129813; AAD38358.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   867 AA;  97133 MW;  DE674A948DE11DCC CRC64;

  Query Match             46.1%;  Score 70.5;  DB 2;  Length 867;
  Best Local Similarity   75.0%;  Pred. No. 0.6;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 35
PAS1_HUMAN
ID   PAS1_HUMAN     STANDARD;      PRT;   870 AA.
AC   Q99814; Q86VA2; Q99630;
DT   15-DEC-1998 (Rel. 37, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2)
DE   (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha)
DE   (HIF-1 alpha-like factor) (HLF).
GN   Name=EPAS1; Synonyms=HIF2A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97152468; PubMed=9000051;
RA   Tian H., McKnight S.L., Russell D.W.;
RT   "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT   selectively expressed in endothelial cells.";
RL   Genes Dev. 11:72-82(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hepatoma;
RX   MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA   Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA   Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT   "Characterization of a subset of the basic-helix-loop-helix-PAS
RT   superfamily that interacts with components of the dioxin signaling
RT   pathway.";
RL   J. Biol. Chem. 272:8581-8593(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP   MUTAGENESIS OF CYS-844.
RX   MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA   Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA   Poellinger L., Fujii-Kuriyama Y.;
RT   "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT   in response to hypoxia: their stabilization and redox signal-induced
RT   interaction with CBP/p300.";
RL   EMBO J. 18:1905-1914(1999).
CC   -!- FUNCTION: Transcription factor involved in the induction of oxygen
CC       regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
CC       the hypoxia response element (HRE) of target gene promoters.
CC       Regulates the vascular endothelial growth factor (VEGF) expression
CC       and seems to be implicated in the development of blood vessels and
CC       the tubular system of lung. May also play a role in the formation
CC       of the endothelium that gives rise to the blood brain barrier.
CC       Potent activator of the Tie-2 tyrosine kinase expression.
CC       Activation seems to require recruitment of transcriptional
CC       coactivators such as CREBPB and probably EP300. Interaction with
CC       redox regulatory protein APEX seems to activate CTAD.
CC   -!- SUBUNIT: Efficient DNA binding requires dimerization wih another
CC       bHLH protein. Heterodimerizes with ARNT. Interacts with CREBBP (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
CC       in placenta, lung and heart. Selectively expressed in endothelial
CC       cells.
CC   -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-531
CC       by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
CC       prolines promote interaction with VHL, initiating rapid
CC       ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-847 by HIF1AN thus
CC       probably abrogating interaction with CREBBP and EP300 and
CC       preventing transcriptional activation (By similarity).
CC   -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U81984; AAB41495.1; -.
DR   EMBL; U51626; AAC51212.1; -.
DR   EMBL; BC051338; AAH51338.1; -.
DR   PDB; 1P97; NMR; A=237-350.
DR   TRANSFAC; T02718; -.
DR   Genew; HGNC:3374; EPAS1.
DR   MIM; 603349; -.
DR   GO; GO:0003705; F:RNA polymerase II transcription factor acti. . .; TAS.
DR   GO; GO:0003713; F:transcription coactivator activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0006366; P:transcription from Pol II promoter; TAS.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
KW   3D-structure; Activator; Angiogenesis; Developmental protein;
KW   DNA-binding; Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW   Transcription regulation.
FT   DNA_BIND     15     27       Basic motif.
FT   DOMAIN       28     68       Helix-loop-helix motif.
FT   DOMAIN       84    154       PAS 1.
FT   DOMAIN      230    300       PAS 2.
FT   DOMAIN      304    347       PAC.
FT   DOMAIN      496    542       NTAD.
FT   DOMAIN      830    870       CTAD.
FT   DOMAIN      474    480       Poly-Ser.
FT   MOD_RES     405    405       Hydroxyproline (By similarity).
FT   MOD_RES     531    531       Hydroxyproline (By similarity).
FT   MOD_RES     840    840       Phosphothreonine (By similarity).
FT   MOD_RES     847    847       3-hydroxyasparagine (By similarity).
FT   MUTAGEN     844    844       C->S: Abolishes hypoxia-inducible
FT                                transcriptional activation of ctaD.
FT   CONFLICT     60     60       A -> E (in Ref. 1).
FT   CONFLICT    539    539       D -> G (in Ref. 2).
FT   CONFLICT    601    601       H -> R (in Ref. 2).
FT   CONFLICT    693    693       D -> N (in Ref. 2).
FT   CONFLICT    716    716       E -> K (in Ref. 2).
FT   CONFLICT    722    722       L -> P (in Ref. 2).
FT   CONFLICT    765    765       F -> L (in Ref. 2).
FT   CONFLICT    769    769       P -> S (in Ref. 2).
FT   CONFLICT    844    844       C -> R (in Ref. 2).
FT   CONFLICT    847    847       N -> K (in Ref. 2).
SQ   SEQUENCE   870 AA;  96458 MW;  4838989598234FC1 CRC64;

  Query Match             46.1%;  Score 70.5;  DB 1;  Length 870;
  Best Local Similarity   75.0%;  Pred. No. 0.61;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        523 ELDLETLAPYIPMDGEDFQL 542


RESULT 36
Q9XTA4
ID   Q9XTA4      PRELIMINARY;      PRT;   870 AA.
AC   Q9XTA4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Endothelial PAS domain protein 1/hypoxia-inducible factor-2
DE   alpha.
GN   Name=EPAS1/HIF2 alpha;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Arterial;
RX   MEDLINE=99255430; PubMed=10320777; DOI=10.1016/S0167-4781(99)00048-2;
RA   Hara S., Kobayashi C., Imura N.;
RT   "Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-
RT   1alpha and -2alpha of bovine arterial endothelial cells.";
RL   Biochim. Biophys. Acta 1445:237-243(1999).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AB018399; BAA78676.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
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```
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   870 AA;  96168 MW;  FEC602E6012D7712 CRC64;

  Query Match             46.1%;  Score 70.5;  DB 2;  Length 870;
  Best Local Similarity   75.0%;  Pred. No. 0.61;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 37
Q9PTB3
ID   Q9PTB3      PRELIMINARY;      PRT;   870 AA.
AC   Q9PTB3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypoxia-inducible factor 2 alpha.
OS   Coturnix coturnix (Common quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=9091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99425185; PubMed=10495286; DOI=10.1016/S0925-4773(99)00144-6;
RA   Elvert G., Lanz S., Kappel A., Flamme I.;
RT   "mRNA cloning and expression studies of the quail homolog of HIF-2
RT   alpha.";
RL   Mech. Dev. 87:193-197(1999).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; AF212989; AAF21052.1; -.
DR   HSSP; Q99814; 1P97.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50888; HLH; 1.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   870 AA;  97803 MW;  086AC8CF1639D77C CRC64;

  Query Match             46.1%;  Score 70.5;  DB 2;  Length 870;
  Best Local Similarity   75.0%;  Pred. No. 0.61;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 38
PAS1_MOUSE
ID   PAS1_MOUSE     STANDARD;      PRT;   874 AA.
AC   P97481; O08787; O55046;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2
DE   alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (MHLF)
DE   (HIF-related factor) (HRF).
GN   Name=Epas1; Synonyms=Hif2a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97152468; PubMed=9000051;
RA   Tian H., McKnight S.L., Russell D.W.;
RT   "Endothelial PAS domain protein 1 (EPAS1), a transcription factor
RT   selectively expressed in endothelial cells.";
RL   Genes Dev. 11:72-82(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Hypothalamus, and Skeletal muscle;
RX   MEDLINE=97272213; PubMed=9113979; DOI=10.1073/pnas.94.9.4273;
RA   Ema M., Taya S., Yokotani N., Sogawa K., Matsuda Y.,
RA   Fujii-Kuriyama Y.;
RT   "A novel bHLH-PAS factor with close sequence similarity to hypoxia-
RT   inducible factor 1alpha regulates the VEGF expression and is
RT   potentially involved in lung and vascular development.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain capillary;
RX   MEDLINE=97321546; PubMed=9178256; DOI=10.1016/S0925-4773(97)00674-6;
RA   Flamme I., Froehlich T., von Reutern M., Kappel A., Damert A.,
RA   Risau W.;
RT   "HRF, a putative basic helix-loop-helix-PAS-domain transcription
RT   factor is closely related to hypoxia-inducible factor-1 alpha and
RT   developmentally expressed in blood vessels.";
RL   Mech. Dev. 63:51-60(1997).
RN   [4]
RP   SEQUENCE OF 846-864, AND MUTAGENESIS OF PRO-530 AND ASN-851.
RX   MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA   Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA   Bruick R.K.;
RT   "FIH-1 is an asparaginyl hydroxylase enzyme that regulates the
RT   transcriptional activity of hypoxia-inducible factor.";
RL   Genes Dev. 16:1466-1471(2002).
RN   [5]
RP   INTERACTION WITH CREBBP, PHOSPHORYLATION SITE THR-844, AND MUTAGENESIS
RP   OF THR-844.
RX   MEDLINE=22075202; PubMed=11983697; DOI=10.1074/jbc.M201307200;
RA   Gradin K., Takasaki C., Fujii-Kuriyama Y., Sogawa K.;
RT   "The transcriptional activation function of the HIF-like factor
RT   requires phosphorylation at a conserved threonine.";
RL   J. Biol. Chem. 277:23508-23514(2002).
RN   [6]
RP   HYDROXYLATION OF ASN-851.
RX   MEDLINE=21682001; PubMed=11823643; DOI=10.1126/science.1068592;
RA   Lando D., Peet D.J., Whelan D.A., Gorman J.J., Whitelaw M.L.;
RT   "Asparagine hydroxylation of the HIF transactivation domain a hypoxic
RT   switch.";
RL   Science 295:858-861(2002).
CC   -!- FUNCTION: Transcription factor involved in the induction of oxygen
CC       regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
CC       the hypoxia response element (HRE) of target gene promoters.
CC       Regulates the vascular endothelial growth factor (VEGF) expression
CC       and seems to be implicated in the development of blood vessels and
```

```
CC       the tubular system of lung. May also play a role in the formation
CC       of the endothelium that gives rise to the blood brain barrier.
CC       Potent activator of the Tie-2 tyrosine kinase expression.
CC       Activation requires recruitment of transcriptional coactivators
CC       such as CREBPB and probably EP300. Interaction with redox
CC       regulatory protein APEX seems to activate CTAD (By similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires dimerization wih another
CC       bHLH protein. Heterodimerizes with ARNT. Interacts with CREBPB.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues, with highest levels
CC       in lung, followed by heart, kidney, brain and liver. Predominantly
CC       expressed in endothelial cells. Also found in smooth muscle cells
CC       of the uterus, neurons, and brown adipose tissue. High expression
CC       in embryonic choroid plexus and kidney glomeruli.
CC   -!- DEVELOPMENTAL STAGE: In day 11 embryo, expression is almost
CC       exclusively seen in endothelial cells of the intersegmental blood
CC       vessels separating the somites, the atrial and ventricular
CC       chambers of the heart, and the dorsal aorta. High expression also
CC       occurs in extra-embryonic membranes. In the developing brain of
CC       day 13 embryo, endothelial cells of the highly vascularized
CC       choroid plexus contain high levels of EPAS1.
CC   -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530
CC       by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
CC       prolines promote interaction with VHL, initiating rapid
CC       ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus
CC       probably abrogating interaction with CREBBP and EP300 and
CC       preventing transcriptional activation.
CC   -!- PTM: Phosphorylated on multiple sites in the CTAD.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U81983; AAB41496.1; -.
DR   EMBL; D89787; BAA20130.1; -.
DR   EMBL; AF045160; AAC12871.1; -.
DR   HSSP; Q16665; 1H2K.
DR   TRANSFAC; T02719; -.
DR   MGD; MGI:109169; Epas1.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   TIGRFAMs; TIGR00229; sensory_box; 2.
DR   PROSITE; PS50888; HLH; FALSE_NEG.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; Angiogenesis; Developmental protein;
KW   Direct protein sequencing; DNA-binding; Hydroxylation;
KW   Nuclear protein; Phosphorylation; Repeat; Transcription regulation.
FT   DNA_BIND     15     27       Basic motif.
FT   DOMAIN       28     68       Helix-loop-helix motif.
FT   DOMAIN       84    154       PAS 1.
FT   DOMAIN      230    300       PAS 2.
FT   DOMAIN      304    347       PAC.
FT   DOMAIN      495    541       NTAD.
FT   DOMAIN      834    874       CTAD.
FT   DOMAIN      471    479       Poly-Ser.
FT   MOD_RES     405    405       Hydroxyproline (By similarity).
FT   MOD_RES     530    530       Hydroxyproline (By similarity).
FT   MOD_RES     844    844       Phosphothreonine.
FT   MOD_RES     851    851       3-hydroxyasparagine.
FT   MUTAGEN     530    530       P->A: Confers transcriptional activity at
FT                                normoxia; when associated with A-851.
FT   MUTAGEN     844    844       T->A: Decreases interaction with CREBBP.
FT   MUTAGEN     851    851       N->A: Confers transcriptional activity at
FT                                normoxia; when associated with A-530.
FT   CONFLICT     25     25       C -> S (in Ref. 2).
FT   CONFLICT    191    191       K -> KS (in Ref. 1).
FT   CONFLICT    439    440       VS -> AA (in Ref. 3).
FT   CONFLICT    463    463       D -> G (in Ref. 3).
FT   CONFLICT    654    654       G -> V (in Ref. 2).
FT   CONFLICT    663    663       A -> P (in Ref. 2).
FT   CONFLICT    669    669       S -> W (in Ref. 1).
FT   CONFLICT    673    673       P -> L (in Ref. 1).
FT   CONFLICT    678    678       P -> L (in Ref. 1).
FT   CONFLICT    725    725       D -> E (in Ref. 3).
FT   CONFLICT    731    731       P -> L (in Ref. 3).
FT   CONFLICT    762    762       A -> G (in Ref. 3).
FT   CONFLICT    786    786       P -> L (in Ref. 3).
FT   CONFLICT    791    791       S -> F (in Ref. 3).
FT   CONFLICT    794    794       S -> N (in Ref. 3).
SQ   SEQUENCE   874 AA;  96712 MW;  A6FFA490AE43640C CRC64;

  Query Match             46.1%;  Score 70.5;  DB 1;  Length 874;
  Best Local Similarity   75.0%;  Pred. No. 0.61;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 39
PAS1_RAT
ID   PAS1_RAT       STANDARD;      PRT;   874 AA.
AC   Q9JHS1;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Endothelial PAS domain protein 1 (EPAS-1) (Hypoxia-inducible factor 2
DE   alpha) (HIF-2 alpha) (HIF2 alpha).
GN   Name=Epas1; Synonyms=Hif2a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21134367; PubMed=11237857; DOI=10.1042/0264-6021:3540531;
RA   Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;
RT   "Perivenous expression of the mRNA of the three hypoxia-inducible
RT   factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";
RL   Biochem. J. 354:531-537(2001).
CC   -!- FUNCTION: Transcription factor involved in the induction of oxygen
CC       regulated genes. Binds to core DNA sequence 5'-[AG]CGTG-3' within
CC       the hypoxia response element (HRE) of target gene promoters.
CC       Regulates the vascular endothelial growth factor (VEGF) expression
CC       and seems to be implicated in the development of blood vessels and
CC       the tubular system of lung. May also play a role in the formation
CC       of the endothelium that gives rise to the blood brain barrier.
CC       Potent activator of the Tie-2 tyrosine kinase expression.
CC       Activation seems to require recruitment of transcriptional
CC       coactivators such as CREBPB and probably EP300. Interaction with
CC       redox regulatory protein APEX seems to activate CTAD (By
CC       similarity).
CC   -!- SUBUNIT: Efficient DNA binding requires dimerization wih another
CC       bHLH protein. Heterodimerizes with ARNT (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
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CC   -!- PTM: In normoxia, is probably hydroxylated on Pro-405 and Pro-530
CC       by EGLN1/PHD1, EGLN2/PHD2 and/or EGLN3/PHD3. The hydroxylated
CC       prolines promote interaction with VHL, initiating rapid
CC       ubiquitination and subsequent proteasomal degradation. Under
CC       hypoxia, proline hydroxylation is impaired and ubiquitination is
CC       attenuated, resulting in stabilization (By similarity).
CC   -!- PTM: In normoxia, is hydroxylated on Asn-851 by HIF1AN thus
CC       probably abrogating interaction with CREBBP and EP300 and
CC       preventing transcriptional activation (By similarity).
CC   -!- PTM: Phosphorylated on multiple sites in the CTAD (By similarity).
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC   -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277828; CAB96612.1; -.
DR   HSSP; Q16665; 1H2K.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 2.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   TIGRFAMs; TIGR00229; sensory_box; 2.
DR   PROSITE; PS50888; HLH; FALSE_NEG.
DR   PROSITE; PS50112; PAS; 2.
KW   Activator; Angiogenesis; Developmental protein; DNA-binding;
KW   Hydroxylation; Nuclear protein; Phosphorylation; Repeat;
KW   Transcription regulation.
FT   DNA_BIND     15     27       Basic motif.
FT   DOMAIN       28     68       Helix-loop-helix motif.
FT   DOMAIN       84    154       PAS 1.
FT   DOMAIN      230    300       PAS 2.
FT   DOMAIN      304    347       PAC.
FT   DOMAIN      495    541       NTAD.
FT   DOMAIN      834    874       CTAD.
FT   DOMAIN      474    479       Poly-Ser.
FT   MOD_RES     405    405       Hydroxyproline (By similarity).
FT   MOD_RES     530    530       Hydroxyproline (By similarity).
FT   MOD_RES     844    844       Phosphothreonine (By similarity).
FT   MOD_RES     851    851       3-hydroxyasparagine (By similarity).
SQ   SEQUENCE   874 AA;  96718 MW;  A1FF08EB24369796 CRC64;

  Query Match             46.1%;  Score 70.5;  DB 1;  Length 874;
  Best Local Similarity   75.0%;  Pred. No. 0.61;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 40
Q6PEU2
ID   Q6PEU2      PRELIMINARY;      PRT;   874 AA.
AC   Q6PEU2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Endothelial PAS domain protein 1.
GN   Name=Epas1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Mammary tumor. Brca1-/fl;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR   EMBL; BC057870; AAH57870.1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0004871; F:signal transducer activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR001067; Nuc_translocat.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS.
DR   Pfam; PF00010; HLH; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00989; PAS; 1.
DR   PRINTS; PR00785; NCTRNSLOCATR.
DR   SMART; SM00353; HLH; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 2.
DR   PROSITE; PS50112; PAS; 2.
SQ   SEQUENCE   874 AA;  96636 MW;  2E6D7603A678EACE CRC64;

  Query Match             46.1%;  Score 70.5;  DB 2;  Length 874;
  Best Local Similarity   75.0%;  Pred. No. 0.61;
  Matches   15;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         12 DLDLEMLAXYIPMD-DDFQL 30
              :|||| ||:||||| :||||
Db        522 ELDLETLAPYIPMDGEDFQL 541


RESULT 41
Q71939
ID   Q71939      PRELIMINARY;      PRT;    71 AA.
AC   Q71939;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
```

```
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Michael N.L.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U24453; AAA79589.1; -.
DR   HSSP; P12506; 1TBC.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      71     71
SQ   SEQUENCE   71 AA;  8307 MW;  A3EFC2840AFF2A50 CRC64;

  Query Match             42.2%;  Score 64.5;  DB 2;  Length 71;
  Best Local Similarity   58.3%;  Pred. No. 0.27;
  Matches   14;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAXYIP 23
              ||||||||||   | :   :|:|
Db         47 YGRKKRRQRRRAPQDSQTYQAYLP 70


RESULT 42
Q71945
ID   Q71945      PRELIMINARY;      PRT;    71 AA.
AC   Q71945;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Michael N.L.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U24454; AAA79595.1; -.
DR   HSSP; P12506; 1TBC.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      71     71
SQ   SEQUENCE   71 AA;  8307 MW;  A3EFC2840AFF2A50 CRC64;

  Query Match             42.2%;  Score 64.5;  DB 2;  Length 71;
  Best Local Similarity   58.3%;  Pred. No. 0.27;
  Matches   14;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAXYIP 23
              ||||||||||   | :   :|:|
Db         47 YGRKKRRQRRRAPQDSQTYQAYLP 70


RESULT 43
Q69628
ID   Q69628      PRELIMINARY;      PRT;    72 AA.
AC   Q69628;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95264414; PubMed=7745674;
RA   Diaz R.S., Sabino E.C., Mayer A., Mosley J.W., Busch M.P.;
RT   "Dual human immunodeficiency virus type 1 infection and recombination
RT   in a dually exposed transfusion recipient. The Transfusion Safety
RT   Study Group.";
RL   J. Virol. 69:3273-3281(1995).
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U11191; AAA78877.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      72     72
SQ   SEQUENCE   72 AA;  8428 MW;  4A00C4BF893D0E86 CRC64;

  Query Match             41.5%;  Score 63.5;  DB 2;  Length 72;
  Best Local Similarity   65.2%;  Pred. No. 0.38;
  Matches   15;  Conservative    2;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRDL-DLEMLAXYI 22
              ||||||||||.| | | |   :|:
Db         47 YGRKKRRQRRRALKDSETHQAYL 69


RESULT 44
O71264
ID   O71264      PRELIMINARY;      PRT;   101 AA.
AC   O71264;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oelrichs R.B., McPhee D.A., Deacon N.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
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CC       promoter (By similarity).
DR   EMBL; AF042102; AAD03212.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   101 AA;  11618 MW;  AE07717D0D3C01E1 CRC64;

  Query Match             40.8%;  Score 62.5;  DB 2;  Length 101;
  Best Local Similarity   58.3%;  Pred. No. 0.76;
  Matches   14;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAXYIP 23
              ||||||||||   | :   :|:|
Db         47 YGRKKRRQRRRAPQDSQTHQIYLP 70


RESULT 45
Q8ADC2
ID   Q8ADC2      PRELIMINARY;      PRT;    86 AA.
AC   Q8ADC2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325;
RA   Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA   Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
RA   Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA   McCutchan F.E.;
RT   "Among 46 near full length HIV type 1 genome sequences from Rakai
RT   District, Uganda, subtype D and AD recombinants predominate.";
RL   AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harris M.E., Birx D.L., Robb M.L.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Lutalo T.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Meehen M., Wawer M.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AF484516; AAN73784.1; -.
DR   HSSP; P04613; 1K5K.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   86 AA;  9905 MW;  01C995B36AE0161A CRC64;

  Query Match             40.5%;  Score 62;  DB 2;  Length 86;
  Best Local Similarity   53.8%;  Pred. No. 0.75;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels   10;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPMDD 26
              ||||||||||           | ||
Db         47 YGRKKRRQRRRS----------PQDD 62


RESULT 46
P88699
ID   P88699      PRELIMINARY;      PRT;    72 AA.
AC   P88699;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat protein (Fragment).
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Quinones-Mateu M.E., Domingo E.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U80465; AAB39115.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
FT   NON_TER      72      72
SQ   SEQUENCE   72 AA;  8342 MW;  ED2C18A34DA4B591 CRC64;

  Query Match             39.9%;  Score 61;  DB 2;  Length 72;
  Best Local Similarity   91.7%;  Pred. No. 0.85;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGRKKRRQRRRD 12
              ||||||:|||||
Db         47 YGRKKRKQRRRD 58


RESULT 47
Q6EK47
ID   Q6EK47      PRELIMINARY;      PRT;   101 AA.
AC   Q6EK47;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
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OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Philpott S.M., Weiser B., Tsoukas C., Foley B., Anastos K.,
RA   Kitchen C., Burger H.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AY314045; AAQ86607.1; -.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   101 AA;  11653 MW;  72F4E0BF83ED5C0E CRC64;

  Query Match             39.5%;  Score 60.5;  DB 2;  Length 101;
  Best Local Similarity   55.6%;  Pred. No. 1.4;
  Matches   15;  Conservative    4;  Mismatches    5;  Indels    3;  Gaps    2;

Qy          1 YGRKKRRQRRR-DLDLEMLAXYIPMDD 26
              ||||||||||   | |  |: :|: :
Db         47 YGRKKRRQRRRPPQDSE--AHQVPLSE 71


RESULT 48
Q72493
ID   Q72493      PRELIMINARY;      PRT;   101 AA.
AC   Q72493;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tat.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96036482; PubMed=7483282;
RA   Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA   Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT   "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT   from primary virus cultures using the polymerase chain reaction.";
RL   Virology 213:80-86(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Salminen M., Koch C., Sanders-Buell E., Ehrenberg P.K., Michael N.L.,
RA   Carr J.K., Burke D.S., McCutchan F.E.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; U26546; AAA86734.1; -.
DR   HSSP; P04610; 1JFW.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   101 AA;  11465 MW;  E951C4A477E3D8FD CRC64;

  Query Match             39.5%;  Score 60.5;  DB 2;  Length 101;
  Best Local Similarity   58.3%;  Pred. No. 1.4;
  Matches   14;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPM 24
              ||||||||||    | | : :|:
Db         47 YGRKKRRQRRR-APPEGLTHQVPL 69


RESULT 49
Q6EG25
ID   Q6EG25      PRELIMINARY;      PRT;   101 AA.
AC   Q6EG25;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bernardin F., Peddada L., Delwart E.L.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AY331290; AAQ97510.1; -.
DR   EMBL; AY331289; AAQ97501.1; -.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
DR   PRINTS; PR00055; HIVTATDOMAIN.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   101 AA;  11686 MW;  AA20EBFCCC7D88D7 CRC64;

  Query Match             38.9%;  Score 59.5;  DB 2;  Length 101;
  Best Local Similarity   48.4%;  Pred. No. 2;
  Matches   15;  Conservative    4;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 YGRKKRRQRRR-DLDLEMLAXYIPMDDDFQL 30
              ||||||||||   | ::  : :|     ||
Db         47 YGRKKRRQRRRAHQDSQIHQVPVPKQPTSQL 77


RESULT 50
Q8ADL8
ID   Q8ADL8      PRELIMINARY;      PRT;    86 AA.
AC   Q8ADL8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tat protein.
GN   Name=tat;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325;
RA   Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA   Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
RA   Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA   McCutchan F.E.;
RT   "Among 46 near full length HIV type 1 genome sequences from Rakai
RT   District, Uganda, subtype D and AD recombinants predominate.";
RL   AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
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RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harris M.E., Birx D.L., Robb M.L.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Lutalo T.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Meehen M., Wawer M.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter (By similarity).
DR   EMBL; AF484504; AAN73676.1; -.
DR   HSSP; P04613; 1K5K.
DR   GO; GO:0042025; C:host cell nucleus; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003723; F:RNA binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001831; IV_Tat.
DR   Pfam; PF00539; Tat; 1.
KW   Activator; Nuclear protein; RNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   86 AA;  9858 MW;  29052AD5D90A8498 CRC64;

  Query Match             38.6%;  Score 59;  DB 2;  Length 86;
  Best Local Similarity   53.8%;  Pred. No. 2;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels   10;  Gaps    1;

Qy          1 YGRKKRRQRRRDLDLEMLAXYIPMDD 26
              ||||||||||           | ||
Db         47 YGRKKRRQRRR----------APPDD 62


Search completed: February  8, 2005, 20:09:56
Job time : 150.947 secs
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